# New Sequences and Sequence Sets in 1995

In database releases over the last ten years, we were able to present annotated GenBank sequences and sometimes sets of sequences in alignment. That is no longer possible—more than 5000 sequences can be pulled up from GenBank using the search words "HIV AND 1995." Some of the sequences are ESTs, some are sequences of antibodies to HIV epitopes, some are accidentally recognized by the search terms and have nothing to do with HIV. Nevertheless, the number of new HIV and SIV sequences is too great to handle as individual files in hard copy or on floppy disks.

Beginning with this issue, we present catalog listings of newly reported sequences, with ample information about the identity of the sequence(s) and how to locate it/them in the gene libraries as well as comments pertaining to the country of origin, subtype, etc. This information, you will find, is much more than can be found in the gene libraries, which of necessity have become increasingly skeletal. In effect, we are playing the role of curators with regard to HIV and HIV-related sequences in the large libraries. The HIV Sequence Database is not copyrighted and therefore this information can be imported into the gene library entries.

The catalogs are arranged by coding sequence, except for central region genes that are kept together. When a study (i.e., publication) reports sequences from two regions of the viral molecule, entries will be found for each in the appropriate tables. Complete genomic sequences are represented in every region. The catalogs will not, however, include a separate entry for every sequence of a given kind in a given study/publication; rather, one sequence will represent the set and accession numbers and other characterizing information are presented in the comments to that representative entry. The database will maintain a master catalog—in electronic form of course—in which every sequence is an entry. In fact, we are in the process of converting all known sequence of HIVs and SIVs into catalog entries. This is an extremely laborious task that will eventually lead to a sequence library maintained as a relational database for the community; it will not be complete for some time.

It is entirely possible that we have overlooked some sequences from 1995. If the sequencers will provide us with the necessary information, as indicated by the catalog entries, we will include their sequences in the catalogs on our Web site (http://hiv-web.lanl.gov). Furthermore, any pertinent information that has been omitted from the comments to a sequence can be quickly added to the Web site copies of these catalogs.

We do include the complete genomic sequence for HIV-1 WEAU because it has become the reference sequence for the molecular immunology component of the database. The full-length IbNG sequence is of special interest because so few complete sequences of non-B subtype viruses are available. Single tables are presented for all HIV2/SIV and SIVAGM sequences that we could identify.

**HIV-1 LTR Sequence Summaries**

| LOCUS | COMMON | ACCESSION | LENGTH | REGION | FIRST AUTHOR | REFERENCE |
|---|---|---|---|---|---|---|
| HIVF12CG | F12CG | Z11530 | 9781 | comp. gen. | Carlini,F. | J. Viral Diseases 1, 40 (1992) |

Comment: HUT-78 cells infected with blood from an AIDS patient were cloned by a group in Rome, Italy. This sequence describes clone F12, which in spite of being taken from an integrated HIV-1 provirus apparently lacking any major deletions, does not release virus particles into the medium. The sequence does appear to have minor deletions, which the authors postulate could affect the correct production of viral proteins at a posttranscriptional level (see ARHR 5, 385 (1989)). Sequence F12CG clusters with subtype B and is closely related to the IIIB strain (97.4% identical to HXB2 overall, 97.6% over gag, 96.4% over pol, and 99.0% identical to HXB2 over env).

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|---|---|---|---|---|---|---|
| HIV1U37267 | C18 | U37267 | 493 | ltr, nef | Deacon,N.J. | Science 270, 988 (1995) |

Comment: Sequences relating to an Australian blood donor infected with HIV-1 and six Australian recipients, all of whom remain symptom free with normal CD4 counts 10 to 14 years after infection. Samples from only the donor, D36 (U37271), and two patients, C18 (U37267, U37270) and C98 (U37268, U37269), appear to have been sequenced. These sequences have similar deletions in the nef gene and in the region of overlap of nef and the U3 region of LTR. The authors point to the importance of NEF or the U3 region of LTR in determining the pathogenicity of HIV-1 and suggest this strain of HIV-1 as a possible basis for a live attenuated vaccine. Presumably subtype B.

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|---|---|---|---|---|---|---|
| S76651 | GER | S76651 | 604 | ltr | Emiliani,S. | ARHR 10: 1751 (1994) |

Comment: Subtype D sequence from a French male patient. The virus is reported to be highly cytopathic, and therefore of interest in comparison to the NDK virus. For the gag p17 sequence, see U11549 (ARHR 10:1043, 1995).

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|---|---|---|---|---|---|---|
| HIV3202A12 | 3202A21 | U34603 | 9636 | comp. gen. | Guillon,C. | ARHR 11, 1537 (1995) |

Comment: Two complete genomes derived from two clones from the same patient, p320, during a study of SI and NSI varients isolated from a single patient. One clone (U34603) is Syncytium Inducing while the other (U34604) is Non Syncytium Inducing. Patient p320 was from Amsterdam and probably harbors subtype B virus.

| | | | | | | |
|---|---|---|---|---|---|---|
| HIVIBNG | IbNg | L39106 | 9201 | comp. gen. | Howard,T.M. | ARHR, in press 1996 |

Comment: This HIV-1 subtype A strain is from a 23 year old asymptomatic male from Ibadan, Nigeria. The isolate was co-cultured in donor PBMCs for two passages before cytoplasmic RNA was harvested and RT-PCR performed to generate 5 overlapping fragments for sequencing. At least 3 separate cloned PCR products were used as sequencing templates for each of the 5 regions. The sequence presented in L39106 is a consensus of all sequencing reactions. The consensus sequence of 6–8 PCR-derived clones from the env gene was discussed in ARHR 10 (12): 1755–1757 (1994). This sequence is one of the few non-subtype B complete genomes. Some unique features were found, including a 16 bp insertion within the Lys-tRNA primer binding site (between the 5' LTR and gag) and a frameshift in the first coding exon of Tat.

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|---|---|---|---|---|---|---|
| HIVTH475A | IIIB-TH | L31963 | 9795 | comp. gen. | Neumann,M. | JVI 69: 2159 (1995) |

Comment: The persistently infected, low-producer human astrocytoma cell line TH4-7-5 was established by multiple rounds of cell cloning following cocultivation of parental 85HG-66 astrocytoma cells with KE37/1-IIIB cells (infected with the IIIB lab strain of HIV-1) as described in AIDS 6: 273 (1992). In this study the entire proviral genome was sequenced from TH4-7-5 cells, and the Rev and Rev responsive element (RRE) were sequenced from progeny virus rescued from TH4-7-5 glial cells into RC-2A monocyte-macrophage leukemia cells. The study indicates that the low-producer status of the TH4-7-5 glial cells is not due to a defect in Rev or the RRE, but due to cellular block of Rev-RRE-dependent regulation. Subtype B sequence.

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|---|---|---|---|---|---|---|
| HIV1U26942 | pNL4-3 | U26942 | 9000 | comp. gen. | Salminen,M.O. | Virology 213, 80 (1995) |

Comment: Resequencing of the complete genome of a subtype B virus, clone pNL4-3, using PCR techniques. The original sequence (M19921) was published by Akio et al. in JVI 59, 284-291 (1986). pNL4-3 is a lab-constructed hybrid of NY5 (5' half) and LAI (3' half); it is an infectious clone.

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|---|---|---|---|---|---|---|
| SIU42720 | Cpzant | U42720 | 8182 | comp. gen. | Vanden,M. | Virology (in press, 1996) |

Comment: The second full sequence of a chimp immunodeficiency virus. Significantly divergent from Cpzgab, however the V3 amino acid sequences are remarkably similar. Approximately equidistant from HIV-1 group M and group O clades. Kindly provided prior to publication by Vanden Haesevelde and Saman, Innogenetics, Belgium.

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|---|---|---|---|---|---|---|
| HIV1U23487 | MANC | U23487 | 9655 | comp. gen. | Zhu,T. | Nature 374, 503 (1995) |

Comment: This sequence ostensibly represents HIV-1 captured by PCR from a 1959 patient known as the 'Manchester Sailor' (Corbitt,G., Bailey,A.S., and Williams,G., Lancet 336:51,(1990)). DNA provided to the Aaron Diamond AIDS Research Center for sequencing yielded this product, which is unexplainedly indistinguishable from contemporary HIV-1 sequences: all of its coding sequences cluster with subtype B sequences (for example, closely to HIVD31, GenBank Accession Number X16109) and do not reveal conspicuous synonymous substitution differences from contemporary samples. Subtype B, from U.K. Serological analysis of the HLA DQalpha marker is in disagreement with similar analysis of the 1959 patient's sample.

| LOCUS | COMMON | ACCESSION | LENGTH | REGION | FIRST AUTHOR | REFERENCE |
|---|---|---|---|---|---|---|

HIV1U13210 JP88 U13210 598 gag Abimiku,A.G. ARHR 10, 1581 (1994)
Comment: Subtype G gag sequence from Nigeria that clusters with previously described sequences from Gabon, Zaire, and Taiwan. Sample JV83, accession number U13212, is a related G subtype gag sequence from Nigeria. For related env sequences, see U13208, U13209, U13210, and U13213. Patient JP88 was an AIDS patient.

HIV127GAG 27GAG L39025 373 gag (p17) Albert,J. JVI 68, 5918 (1994)
Comment: Sequences from a Swedish male IV-drug user and a female he allegedly raped. B subtype gag and pol sequences were derived from uncultured PBMCs. The study concludes that the viral sequences from the two individuals were closely epidemiologically linked. Other gag sequences from the study have accession numbers L39044, L39045–L39058. Pol sequences from the study have numbers L39021–L39024, L39026–L39043, L39045–L39048.

HIV1U21096 94–11643 U21096 256 gag Arnold,C. ARHR 11, 427 (1995)
Comment: At least five sequence subtypes found in the U.K.—A, B, C, D and A/E. The subtype A – A/E samples were taken from immigrants, however the subtype C and D cases may represent second-generation transmissions in the U.K. This PBL sequence and gag-pol (U21124) and env (U21109) sequences establish the A/E subtype for sample 94–11643. Other samples in the study are: 93–08020, a subtype B (U21095, U21122, U21100); 93–43424, a subtype D (U21106, 21136, U21098); 93–00333 and 93–00513, a subtype C (Z33479, U21099); 94–31296, a subtype A (U21097). Editor's note: no pure A sequence was reported for env.

HIV1U21124 94–11643 U21124 419 gag, pol Arnold,C. ARHR 11, 427 (1995)
Comment: At least five sequence subtypes found in the U.K.—A, B, C, D and A/E. The subtype A— A/E samples were taken from immigrants, however the subtype C and D cases may represent second-generation transmissions in the U.K. This PBL sequence and gag (U21096) and env (U21109) sequences establish the A/E subtype for sample 94–11643. Other samples in the study are: 93–08020, a subtype B (U21095, U21122, U21100); 93–43424, a subtype D (U21106, 21136, U21098); 93–00333 and 93–00513, a subtype C (Z33479, U21099); 94–31296, a subtype A (U21097). Editor's note: no pure A sequence was reported for env.

HIVGAGB GAGB Z33475 242 gag Barlow,K.L. JVI Methods 52 , 65 (1995)
Comment: Seven gag fragment sequences, part of a U.K. study of false negatives using the Roche-Amplicor test. Accession numbers Z33474–Z33480. Z33479 appears to be a C subtype sequence (see Arnold et al., ARHR 11:427, 1995); the others are presumably B subtype sequences.

HIV1U07238 Kon U07238 861 gag Becker,M.L. ARHR 11, 1265 (1995)
Comment: Fourteen samples from southern Africa (Mozambique, South Africa, Zambia and Malawi) were studied over portions of env and gag coding sequences. Subtype B and D sequences were also uncovered, though the majority were subtype C. Related sequence accession numbers are U07011–U07018, U06716–U06719, and U07237–U07237.

HIVF12CG F12CG Z11530 9781 comp. gen. Carlini,F. J. Viral Diseases 1, 40 (1992)
Comment: HUT-78 cells infected with blood from an AIDS patient were cloned by a group in Rome, Italy. This sequence describes clone F12, which in spite of being taken from an integrated HIV-1 provirus apparently lacking any major deletions, does not release virus particles into the medium. The sequence does appear to have minor deletions, which the authors postulate could affect the correct production of viral proteins at a posttranscriptional level (see ARHR 5, 385 (1989)). Sequence F12CG clusters with subtype B and is closely related to the IIIB strain (97.4% identical to HXB2 overall, 97.6% over gag, 96.4% over pol, and 99.0% identical to HXB2 over env).

HDV1GAG HDV1GAG X84329 513 gag Cohen,J.H.M. Unpublished
Comment: A partial gag sequence, no publication referenced in GenBank entry, not much information available. Most likely subtype O—the unpublished paper cited in the GenBank entry is entitled "A novel HIV1-O strain illustrates the diversity of the O group"—and likely from France, as the first author is based there. On the other hand, there is a 1995 article in Lancet that appears to be related (Lancet 345, 856 (1995)) and which suggests that this is not an O subtype. See two related env sequences, accession numbers X84327 and X84328.

HIVY1GA01 Y101 Z47476 393 gag Cornelissen,M. JVI 69, 1810 (1995)
Comment: Sequences from two donor-recipient pairs The first donor and recipient are called "H" (Z47495–Z47504) and "O" (Z47485–Z47494) respectively, and the second are called "Y" (Z47476–Z47484) and "X" (Z47456–Z47465). The issue of intrapatient selection of syncytium- and non-syncytium-inducing virus phenotypes following transmission was addressed by studying two cases of accidental transmission. The authors conclude that suppression of SI viruses can be accomplished following the development of HIV-specific immunity and that the ability to suppress SI viruses does not prevent the development of immunodeficiency. All sequences presumably subtype B, all patients presumably residents of the Netherlands.

HIV3202A12 3202A21 U34603 9636 comp. gen. Guillon,C. ARHR 11, 1537 (1995)
Comment: Two complete genomes derived from two clones from the same patient, p320, during a study of SI and NSI varients isolated from a single patient. One clone (U34603) is Syncytium Inducing while the other (U34604) is Non Syncytium Inducing. Patient p320 was from Amsterdam and probably harbors subtype B virus.

HIVIBNG IbNg L39106 9201 comp. gen. Howard,T.M. ARHR, in press 1996
Comment: This HIV-1 subtype A strain is from a 23 year old asymptomatic male from Ibadan, Nigeria. The isolate was co-cultured in donor PBMCs for two passages before cytoplasmic RNA was harvested and RT-PCR performed to generate 5 overlapping fragments for sequencing. At least 3 separate cloned PCR products were used as sequencing templates for each of the 5 regions. The sequence presented in L39106 is a consensus of all sequencing reactions. The consensus sequence of 6–8 PCR-derived clones from the env gene was discussed in ARHR 10 (12): 1755–1757 (1994). This sequence is one of the few non-subtype B complete genomes. Some unique features were found, including a 16 bp insertion within the Lys-tRNA primer binding site (between the 5' LTR and gag) and a frameshift in the first coding exon of Tat.

HIV1U19433 BR19C U19433 311 gag Janini,L.M. Unpublished
Comment: Confirmation of HIV-1 homotypic dual infections and phylogenetic analysis of the contributing subtypes. Accession numbers U19411-U19458. U19412 is pol from 7932, U19413 is pol from 7934, U19414 is pol from 7936, U19415 is pol from 7942, U19416 is pol from 7944, U19417 is pol from 7946, U19418 is pol from 8615, U19419 is pol from 8623, U19420 is pol from 8625, U19421 is pol from 8629, U19422 is pol from 8633, U19423 is pol from 8635, U19424 is pol from BR1, U19425 is pol from BR11, U19426 is pol from BR12, U19427 is pol from BR13, U19428 is pol from BR15, U19429 is pol from BR16, U19430 is pol from BR17, U19431 is pol from BR18, U19432-U19433 are pol and gag from BR19c, U19434-U19435 are pol and gag from BR19d, U19436 is pol from BR2, U19437-U19438 are pol and gag from BR20c, U19439-U19440 are pol and gag from BR20d, U19441 is pol from BR21, U19442-U19443 are pol and gag from BR22d, U19444-U19447 are pol and gag from BR22f, U19446 is pol from BR23, U19447 is pol from BR24, U19448 is pol from BR25, U19449 is pol from BR3, U19450-U19451 are pol ang gag from BR30c, U19452 is pol from BR4, U19453-U19453 are pol and gag from BR5b, U19455-U19456 are pol and gag from BR5f, U19457 is pol from BR7 and U19458 is pol from BR9.

HIV1U32123 U32123 355 gag (p17) Kasper,P. ARHR 11: 1197 (1995)
Comment: Gag p17 subtype B sequences from simultaneously infected German individuals with hemophilia. Accession numbers U32123-U32149. Env V3 sequences were previously analyzed (Kasper et al., ARHR 10: 1669,1994; accession numbers S76444, S76446).

HIV117022G SE7022G L41179 412 gag (p17) Leitner,T.K. ARHR 11: 995 (1995)
Comment: Two unrelated individuals who immigrated to Sweden from Zaire had concordant env and gag sequences, which provisionally define a new subtype J. L41176-L41177 are env sequences, L41178-L41179 are gag. Subtype J, Zaire (Sweden).

HIV16165G SE6165G L40752 356 gag (p17) Leitner,T.K. Virology 209: 136 (1995)
Comment: In this study three Swedish HIV-1 transmission chains of subtypes other than subtype B were characterized. The three index cases were African men. Gag and env V3 regions were directly sequenced from uncultured lymphocytes. One group harbored subtype D, another subtype G and the third a recombinant gag-D/env-A subtype. The culture phenotype of virus (SI or NSI) correlated with the clinical stage of the infected individual suggesting that the correlation between biological phenotype and V3 genotype that has been established for subtype B variants may also be valid for other subtypes. L40743-L40751 env; L40752-L40760 gag; L40761-L40763 pol. Subtypes G, D and gag-D/env-A (recombinant) from Sweden.

HIV1U24706 BCF01B U24706 400 gag (p24) Loussert,I. JVI 69: 5640 (1995)
Comment: Sequences encoding Gag p24 and the Env C2-V3 region were obtained from seven patients who were seronegative with ELISA detection kits and had atypical Western blot reactivity. Sequence analyses showed that all of these strains were group O. All seven patients had Cameroonian origins but were living in France at the time the blood samples were taken. Genetic distances between sequences from available group O isolates were generally comparable to those observed in M intersubtype sequence comparisons. U24562-U24568 env; U24706-U24712 gag. Group O, from France.

HIVG1C101 114 Z47903 243 gag Mulder,G.A. JVI 69: 2285 (1995)
Comment: Three mother-child pairs were studied. For pair 114 the infant was HIV positive at birth, for pair 127 the infant became positive 6 weeks after birth and the infant of pair 564 became positive 30 months after birth. Mothers 127 and 114 were seropositive before giving birth. Mother 564 seroconverted after delivery and the infant was infected via breast-feeding. For V3 and p17gag sequences, maternal intrasample variability, including the first seropositive sample of the seroconverted mother, was much higher than infant intrasample variability. In each case the infant was infected by a minor variant present in the maternal sequences. The sequences of the env and gag genes did not identify a particular time of mother-to-child transmission. L21111-L21153 are infant 114 env subtype B from the Netherlands; L21028-L21110 are mother 114 env subtype B from the Netherlands; Z47817-Z47832 are infant 127 env subtype G from the Netherlands; Z47833-Z47880 are mother 127 env subtype G from the Netherlands; Z47881 is child 564 env subtype A from Rwanda; Z47882-Z47902 are mother 564 env subtype A from Rwanda (Mulder-Kampinga et al., J. Gen. Virol. 74:1747, 1993); Gag gene sequences from mother/child pairs are available in Genbank accession numbers Z47903-Z47911; Z47912-Z47928; Z47929-Z47935; Z47936-Z47950.

HIVTH475A IIIB-TH L31963 9795 comp. gen. Neumann,M. JVI 69: 2159 (1995)
Comment: The persistently infected, low-producer human astrocytoma cell line TH4-7-5 was established by multiple rounds of cell cloning following cocultivation of parental 85HG-66 astrocytoma cells with KE37/1-IIIB cells (infected with the IIIB lab strain of HIV-1) as described in AIDS 6: 273 (1992). In this study the entire proviral genome was sequenced from TH4-7-5 cells, and the Rev and Rev responsive element (RRE) were sequenced from progeny virus rescued from TH4-7-5 glial cells into RC-2A monocyte-macrophage leukemia cells. The study indicates that the low-producer status of the TH4-7-5 glial cells is not due to a defect in Rev or the RRE, but due to cellular block of Rev-RRE-dependent regulation. Subtype B sequence.

HIV1GA14 GA14 Z29693 441 gag Rojas,J.M. Virus Res. 31, 331 (1994)
Comment: Nine Spanish subtype B sequences (Z29693-Z29701) from different patients. Rojas et al. identified two distint lineages within the cohort. One lineage is related to SF-2/RF and is epidemiologically linked to male homosexuals, while the second is related to III-B which is linked to intravenous drug users. For related sequences see Z29681-Z29692 and Z29919.

HIV1U26942 pNL4-3 U26942 9000 comp. gen. Salminen,M.O. Virology 213, 80 (1995)
Comment: Resequencing of the complete genome of a subtype B virus, clone pNL4-3, using PCR techniques. The original sequence (M19921) was published by Akio et al. in JVI 59, 284-291 (1986). pNL4-3 is a lab-constructed hybrid of NY5 (5' half) and LAI (3' half); it is an infectious clone.

SIU42720 Cpzant U42720 8182 comp. gen. Vanden,M. Virology (in press, 1996)
Comment: The second full sequence of a chimp immunodeficiency virus. Significantly divergent from Cpzgab, however the V3 amino acid sequences are remarkably similar. Approximately equidistant from HIV-1 group M and group O clades. Kindly provided prior to publication by Vanden Haesevelde and Saman, Innogenetics, Belgium.

HIVH1C C, I1 L42013 231 gag Voevodin,A. ARHR 12: 641 (1996)
Comment: Subtype B and C sequences from India and from Indian and Ethiopian expatriates in Kuwait. This entry, I1, is a subtype C sequence from Bihar, India. Accession numbers L42013–L42014, L42016–L42019, L42022. All are C subtype except L42014 (I2), which is subtype B.

HIV1U29413 4-6 U29413 1500 gag Yoshimura,F.K. Unpublished (1995)
Comment: 41 sequences of the gag region, origin and subtype unknown. According to the GenBank entry, the unpublished paper is entitled "Intrapatient variation of gag can be as divergent as env sequences".

HIVM9S1 HIVM9S1 L21518 303 gag Zhu,T. Science 261, 1179 (1993)
Comment: This study included 369 sequences from five HIV-1 seroconverters, with viral phenotypes found to be uniformly macrophage-tropic and non-syncytium-inducing. Furthermore, the viruses were genotypically homogeneous within each patient, although a common signature sequence was not discernible among transmitted viruses. In the two cases where sexual partners were also studied, the sequences of the transmitted viruses matched best with minor variants in the blood of the transmitters. There was also a stronger pressure to conserve sequences in gp120 than in gp41, nef, and p17, suggesting that a selective mechanism is involved in transmission. Sequences for the entire set of 369 sequences from these five patients have accession numbers: L21224-L21591, L24161-L24162. Env and nef gene sequences are also available. Subtype B, from U.S.

HIV1U23487 MANC U23487 9655 comp. gen. Zhu,T. Nature 374, 503 (1995)
Comment: This sequence ostensibly represents HIV-1 captured by PCR from a 1959 patient known as the 'Manchester Sailor' (Corbitt,G., Bailey,A.S., and Williams,G., Lancet 336:51,(1990)). DNA provided to the Aaron Diamond AIDS Research Center for sequencing yielded this product, which is unexplainedly indistinguishable from contemporary HIV-1 sequences: all of its coding sequences cluster with subtype B sequences (for example, closely to HIVD31, GenBank Accession Number X16109) and do not reveal conspicuous synonymous substitution differences from contemporary samples. Subtype B, from U.K. Serological analysis of the HLA DQalpha marker is in disagreement with similar analysis of the 1959 patient's sample.

| LOCUS | COMMON | ACCESSION | LENGTH | REGION | FIRST AUTHOR | REFERENCE |
|---|---|---|---|---|---|---|
| HIV14771PO | 4771PO | L39021 | 635 | pol | Albert,J. | JVI 68, 5918 (1994) |

Comment: Sequences from a Swedish male IV-drug user and a female he allegedly raped. B subtype gag and pol sequences were derived from uncultured PBMCs. The study concludes that the viral sequences from the two individuals were closely epidemiologically linked. Other pol sequences from the study have accession numbers L39022–L39024, L39026–L39043, L39045–L39048. Gag p17 sequences from the study are L39025, L39044, L39045–L39058.

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|---|---|---|---|---|---|---|
| HIV1U21124 | 94–11643 | U21124 | 419 | gag, pol | Arnold,C. | ARHR 11, 427 (1995) |

Comment: At least five sequence subtypes found in the U.K.—A, B, C, D and A/E. The subtype A— A/E samples were taken from immigrants, however the subtype C and D cases may represent second-generation transmissions in the U.K. This PBL sequence and gag (U21096) and env (U21109) sequences establish the A/E subtype for sample 94–11643. Other samples in the study are: 93–08020, a subtype B (U21095, U21122, U21100); 93–43424, a subtype D (U21106, 21136, U21098); 93–00333 and 93–00513, a subtype C (Z33479, U21099); 94–31296, a subtype A (U21097). Editor's note: no pure A sequence was reported for env.;

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| HIVF12CG | F12CG | Z11530 | 9781 | comp. gen. | Carlini,F. | J. Viral Diseases 1, 40 (1992) |

Comment: HUT-78 cells infected with blood from an AIDS patient were cloned by a group in Rome, Italy. This sequence describes clone F12, which in spite of being taken from an integrated HIV-1 provirus apparently lacking any major deletions, does not release virus particles into the medium. The sequence does appear to have minor deletions, which the authors postulate could affect the correct production of viral proteins at a posttranscriptional level (see ARHR 5, 385 (1989)). Sequence F12CG clusters with subtype B and is closely related to the IIIB strain (97.4% identical to HXB2 overall, 97.6% over gag, 96.4% over pol, and 99.0% identical to HXB2 over env).

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|---|---|---|---|---|---|---|
| HIV3202A12 | 3202A21 | U34603 | 9636 | comp. gen. | Guillon,C. | ARHR 11, 1537 (1995) |

Comment: Two comp. gen.s derived from two clones from the same patient, p320, during a study of SI and NSI varients isolated from a single patient. One clone (U34603) is Syncytium Inducing while the other (U34604) is Non Syncytium Inducing. Patient p320 was from Amsterdam and probably harbors subtype B virus.

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|---|---|---|---|---|---|---|
| HIV1RET1 | RET1 | Z31354 | 1299 | pol | Gurusinghe,A.D. | J. Med. Virol. 46, 238–243 (1995) |

Comment: Subtype B. Sequential human immunodeficiency virus type 1 (HIV-1) isolates were obtained over a 29-month period from a person before, during, and after AZT therapy. DNA sequence analysis of polymerase chain-amplified reverse-transcriptase gene showed a gradual accumulation of mutations to peak resistance (IC50 2.13 microM AZT) in association with mutations at codons 44, 210, and 369, as well as at 41, 67, 70, and 215. Eight months after cessation of AZT therapy, when an HIV-1 isolate from the patient was again sensitive to AZT, these mutations had all returned to the pretherapy sequence. Other accession numbers are Z31020, Z31355, Z31365–Z31367, Z31374.

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|---|---|---|---|---|---|---|
| HIV1RTPX | AZT34 | Z37142 | 1719 | pol | Hooker,D.J. | Unpublished |

Comment: A mutation from Leu to Trp at position 210 in reverse transcriptase contributes to high-level AZT resistance. See also Z37143.

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|---|---|---|---|---|---|---|
| HIVIBNG | IbNg | L39106 | 9201 | comp. gen. | Howard,T.M. | ARHR, in press 1996 |

Comment: This HIV-1 subtype A strain is from a 23 year old asymptomatic male from Ibadan, Nigeria. The isolate was co-cultured in donor PBMCs for two passages before cytoplasmic RNA was harvested and RT-PCR performed to generate 5 overlapping fragments for sequencing. At least 3 separate cloned PCR products were used as sequencing templates for each of the 5 regions. The sequence presented in L39106 is a consensus of all sequencing reactions. The consensus sequence of 6–8 PCR-derived clones from the env gene was discussed in ARHR 10 (12): 1755–1757 (1994). This sequence is one of the few non-subtype B comp. gen.s. Some unique features were found, including a 16 bp insertion within the Lys-tRNA primer binding site (between the 5' LTR and gag) and a frameshift in the first coding exon of Tat.

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|---|---|---|---|---|---|---|
| HIV16166P | SE6165P | L40761 | 676 | pol (rt) | Leitner,T.K. | Virology 209: 136 (1995) |

Comment: In this study three Swedish HIV-1 transmission chains of subtypes other than subtype B were characterized. The three index cases were African men. Gag and env V3 regions were directly sequenced from uncultured lymphocytes. One group harbored subtype D, another subtype G and the third a recombinant gag-D/env-A subtype. The culture phenotype of virus (SI or NSI) correlated with the clinical stage of the infected individual suggesting that the correlation between biological phenotype and V3 genotype that has been established for subtype B variants may also be valid for other subtypes. L40743-L40751 env; L40752-L40760 gag; L40761-L40763 pol. Subtypes G, D and gag-D/env-A (recombinant) from Sweden.

HIV106RT01 106RT01 U14786 204 pol Najera,I. JVI 69: 23 (1995)
Comment: The sequences of two pol gene regions (codons 41 to 108 and 181 to 219 of reverse transcriptase) from 60 HIV-1 samples obtained directly from primary lymphocytes from infected individuals in Spain are reported. Twenty-five of the samples were from patients not exposed to antiretroviral compounds and 35 were from patients treated with AZT and/or DDI reverse transcriptase inhibitors. Mutations in codons previously shown to contibute to AZT resistance (for example Lys 70 -> Arg 70) were found in both treated and untreated patients, demonstrating the pre-existence of such mutations before antiretroviral therapy. This study also included sequencing numerous clones from 3 of the individuals (GenBank entries unavailable at this time) in order to estimate mutation frequencies. Sequences for the entire set have accession numbers U14786-U14903. Presumably subtype B.

HIVTH475A IIIB-TH L31963 9795 comp. gen. Neumann,M. JVI 69: 2159 (1995)
Comment: The persistently infected, low-producer human astrocytoma cell line TH4-7-5 was established by multiple rounds of cell cloning following cocultivation of parental 85HG-66 astrocytoma cells with KE37/1-IIIB cells (infected with the IIIB lab strain of HIV-1) as described in AIDS 6: 273 (1992). In this study the entire proviral genome was sequenced from TH4-7-5 cells, and the Rev and Rev responsive element (RRE) were sequenced from progeny virus rescued from TH4-7-5 glial cells into RC-2A monocyte-macrophage leukemia cells. The study indicates that the low-producer status of the TH4-7-5 glial cells is not due to a defect in Rev or the RRE, but due to cellular block of Rev-RRE-dependent regulation. Subtype B sequence.

HIV1U19411 7930 U19411 297 pol Pieniazek,D. Emerg. Inf. Dis. 1:86 (1995)
Comment: Confirmation of HIV-1 homotypic dual infections and phylogenetic analysis of the contributing subtypes. Accession numbers U19411-U19458.omment: Confirmation of HIV-1 homotypic dual infections and phylogenetic analysis of the contributing subtypes. Accession numbers U19411-U19458. U19412 is pol from 7932, U19413 is pol from 7934, U19414 is pol from 7936, U19415 is pol from 7942, U19416 is pol from 7944, U19417 is pol from 7946, U19418 is pol from 8615, U19419 is pol from 8623, U19420 is pol from 8625, U19421 is pol from 8629, U19422 is pol from 8633, U19423 is pol from 8635, U19424 is pol from BR1, U19425 is pol from BR11, U19426 is pol from BR12, U19427 is pol from BR13, U19428 is pol from BR15, U19429 is pol from BR16, U19430 is pol from BR17, U19431 is pol from BR18, U19432-U19433 are pol and gag from BR19c, U19434-U19435 are pol and gag from BR19d, U19436 is pol from BR2, U19437-U19438 are pol and gag from BR20c, U19439-U19440 are pol and gag from BR20d, U19441 is pol from BR21, U19442-U19443 are pol and gag from BR22d, U19444-U19447 are pol and gag from BR22f, U19446 is pol from BR23, U19447 is pol from BR24, U19448 is pol from BR25, U19449 is pol from BR3, U19450-U19451 are pol ang gag from BR30c, U19452 is pol from BR4, U19453-U19453 are pol and gag from BR5b, U19455-U19456 are pol and gag from BR5f, U19457 is pol from BR7 and U19458 is pol from BR9.

HIV1U26942 pNL4-3 U26942 9000 comp. gen. Salminen,M.O. Virology 213, 80 (1995)
Comment: Resequencing of the complete genome of a subtype B virus, clone pNL4-3, using PCR techniques. The original sequence (M19921) was published by Akio et al. in JVI 59, 284-291 (1986). pNL4-3 is a lab-constructed hybrid of NY5 (5' half) and LAI (3' half); it is an infectious clone.

HIVU45331 U45331 362 pol Sheehy,N. Unpublished
Comment: Accession numbers U45331–U45375. Env sequences are also part of the study, accession numbers U45376–U45420. Presumably subtype B.

HIV1U28646 HXBC U28646 1700 pol Tachedjian,G. Virology 212, 58 (1995)
Comment: Eight subtype B sequences from two strains, PD (U28648-U28652) and HX (U28646 U28647 U28653), used during an evaluation of foscarnet-resistant strains of HIV-1. Tachedjian et al. found that foscarnet-resistant strains had unique substitutions in the reverse transcriptase coding region. They determined that foscarnet resistance is likely to be mediated through an altered interaction of a mutant reverse transcriptase enzyme with the template strand of the template primer, which distorts the geometry of the polymerase active site and thereby decreases foscarnet binding.

SIU42720 Cpzant U42720 8182 comp. gen. Vanden,M. Virology (in press, 1996)
Comment: The second full sequence of a chimp immunodeficiency virus. Significantly divergent from Cpzgab, however the V3 amino acid sequences are remarkably similar. Approximately equidistant from HIV-1 group M and group O clades. Kindly provided prior to publication by Vanden Haesevelde and Saman, Innogenetics, Belgium.

HIV1U31385 RJ9434 U31385 457 pol Yamaguchi,K. Biochim. Biophys. Acta. 1253, 136 (1995)
Comment: Twenty-eight sequences (U31385-U31412) used in an investigation to determine if proteinase inhibitor resistance-conferring amino-acid substitutions occur in HIV strains before the application of selective pressure. Yamaguchi et al. found that significant variation occurs in the HIV-1 proteinase gene but pre-existing highly proteinase-resistant strains are uncommon. Presumably subtype B sequences from the U.S.

HIV1U23487 MANC U23487 9655 comp. gen. Zhu,T. Nature 374, 503 (1995)
Comment: This sequence ostensibly represents HIV-1 captured by PCR from a 1959 patient known as the 'Manchester Sailor' (Corbitt,G., Bailey,A.S., and Williams,G., Lancet 336:51,(1990)). DNA provided to the Aaron Diamond AIDS Research Center for sequencing yielded this product, which is unexplainedly indistinguishable from contemporary HIV-1 sequences: all of its coding sequences cluster with subtype B sequences (for example, closely to HIVD31, GenBank Accession Number X16109) and do not reveal conspicuous synonymous substitution differences from contemporary samples. Subtype B, from U.K. Serological analysis of the HLA DQalpha marker is in disagreement with similar analysis of the 1959 patient's sample.

| LOCUS | COMMON | ACCESSION | LENGTH | REGION | FIRST AUTHOR | REFERENCE |
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HIVF12CG F12CG Z11530 9781 comp. gen. Carlini,F. J. Viral Diseases 1, 40 (1992)
Comment: HUT-78 cells infected with blood from an AIDS patient were cloned by a group in Rome, Italy. This sequence describes clone F12, which in spite of being taken from an integrated HIV-1 provirus apparently lacking any major deletions, does not release virus particles into the medium. The sequence does appear to have minor deletions, which the authors postulate could affect the correct production of viral proteins at a posttranscriptional level (see ARHR 5, 385 (1989)). Sequence F12CG clusters with subtype B and is closely related to the IIIB strain (97.4% identical to HXB2 overall, 97.6% over gag, 96.4% over pol, and 99.0% identical to HXB2 over env).

HIV1U11126 H1D16TAT U11126 285 tat Diaz,R.S. JVI 69, 3273 (1995)
Comment: Set of 86 sequences of tat and env from a study involving three infants that received contaminated blood. Recipient 1 (R1) and recipient 2 (R2) each received blood from different donors; a third recipient (DR) received blood from both donors and became dually infected. Sequence DR106 (U11136), from recipient DR, is an apparent recombinant of sequences from the separate donors. GenBank accession numbers U11124-U11209. Donors and recipients all presumably American, sequences all subtype B. More details are available on 1995 compendium page III-119, entry number 82.

HIV11883 1188-3 U41704 285 vpR Ge,Y.C. ARHR (in press, 1996)
Comment: Thirteen clones from eight HIV-infected Australian IV-drug users and seven clones from two long-term non-progressors were studied for length variation in the vpR coding sequence. The majority of samples displayed in-frame deletions or insertions, relative to reference strains, that did not abrogate protein function. All sequences in the study appear to be subtype B vpR sequences. Accession numbers for the eight IV-drug users, patients 710, 890, 891, 894, 896, Lifi, VR and 1188, are U41704-U41706, U41708-U41713, U41717-U41718, U41722-U41723. Accession numbers for the two long-term non-progressors, LW and JW, are U41707, U41714-U41716, U41719-U41721.

HIV3202A12 3202A21 U34603 9636 comp. gen. Guillon,C. ARHR 11, 1537 (1995)
Comment: Two complete genomes derived from two clones from the same patient, p320, during a study of SI and NSI varients isolated from a single patient. One clone (U34603) is Syncytium Inducing while the other (U34604) is Non Syncytium Inducing. Patient p320 was from Amsterdam and probably harbors subtype B virus.

HIVIBNG IbNg L39106 9201 comp. gen. Howard,T.M. ARHR, in press 1996
Comment: This HIV-1 subtype A strain is from a 23 year old asymptomatic male from Ibadan, Nigeria. The isolate was co-cultured in donor PBMCs for two passages before cytoplasmic RNA was harvested and RT-PCR performed to generate 5 overlapping fragments for sequencing. At least 3 separate cloned PCR products were used as sequencing templates for each of the 5 regions. The sequence presented in L39106 is a consensus of all sequencing reactions. The consensus sequence of 6–8 PCR-derived clones from the env gene was discussed in ARHR 10 (12): 1755–1757 (1994). This sequence is one of the few non-subtype B complete genomes. Some unique features were found, including a 16 bp insertion within the Lys-tRNA primer binding site (between the 5' LTR and gag) and a frameshift in the first coding exon of Tat.

HIVU47602 U47602 232 tat Hutto,C. Unpublished
Comment: Accession numbers U47602–U47613. No information.

HIV1U30730 50824–02 U30730 276 rev, env (gp41) Iversen,A.K.N. JVI 69, 5743 (1995)
Comment: This study substituted four complete env genes isolated from the PBMC of an asymptomatic patient 4.5 years after infection into the replication-competent NL4–3 provirus. Despite encoding full-length open reading frames for gp120 and gp41 and the second coding exon of tat and rev, each chimera was replication defective. Site-directed mutagenesis of codon 78 in the Rev activation domain (from a hitherto unique Ile, to the subtype B consensus Leu) partially restored infectivity for two of three chimeras tested. Similarly, mutagenesis of rev codon 78 of NL4–3 from Leu to Ile partially attenuated this virus. The authors also examined conservation of the Rev activation domain within and among long-term survivors (LTS) and patients with AIDS, as well as T-cell-line-adapted strains of HIV-1. Putative attenuating mutations were found in a minority of sequences from all five LTS and two of four patients with AIDS. Of the 11 T-cell-line-adapted viruses examined, none had these changes. Sequence set accession numbers U30730–U30786.

HIVU45960 JR-CSF 17.11 U45960 3211 vpu, env, nef Klasse,P.J. ARHR 12: 347 (1996)
Comment: Syncytium-inducing mutant clone of isolate JR-CSF. Subtype B.

HIVHN0008 HN0008 Z68505 276 vpu Kuiken,L. J. Gen. Virol. In press (1996)
Comment: Title = "Consistent risk group-associated differences in HIV-1 vpr, vpu and V3 sequences despite independent evolution". This is a set of 117 vpu and envelope V3 region sequences from Dutch, Scottish and German patients belonging to different risk groups. GenBank accession numbers for the complete set are Z68505, Z68508-Z68616, and Z68687-Z68693.

HIV1BZ126A BZ126 L22082 3312 tat, rev, vpu, env, nef Louwagie,J. ARHR 10, 561 (1994)
Comment: Env subtype F sequence from Brazil. Part of a study of twenty-one seropositive Brazilians sampled for virus in 1989–1990. B and F subtype sequences were recovered. BZ200 (L22088) and BZ167 (L22087) are B subtype sequences, BZ163 (L22085) and BZ162 (L22084) are other F subtype sequences. The subtype B V3-loop crown sequences were unusual, as has been found for other Brazilian sequences. The BZ126 gag sequence presented in L22083, does not group with subtype F as it did in the publication. Instead it appears to be an A/C recombinant, suggesting a data entry mixup. Accession numbers L11751–L11754 are related.

HIV1SE364A SN364 L22944 3110 tat, rev, vpu, env, nef Louwagie,J.J. JVI 69, 263 (1995)
Comment: Subtype C sequence from Senegal. Full-length env gp160 sequences were obtained from isolates from 8 African countries. Subtype A, C, D, and G sequences are reported. Samples were collected between 1989 and 1991. ZM184 was most closely related to subtype A sequences, but distant enough to warrant an "unclassified" designation. Accession numbers L22939–L22957, L23064, L23065.

HIV1U24443 3799(09–93) U24443 1379 vpr, vif, tat, rev, vpu Michael,N.L. JVI 69, 4228 (1995)
Comment: These sequences represent a 5-year time span within one patient. Patient 3799 became HIV+ via a blood transfusion in 1982. She has remained asymptomatic since that time. The blood donor and two other recipients have all died of AIDS. 3799 is seroreactive to HIV-1 antigens but continually HIV culture negative. Her CD4+ T-cell count hovers around 399 cells per microliters. Long terminal repeat region sequences indicate normal basal and Tat-mediated promoter activities. There is a low frequency of defective nef genes. In contrast, the vif, vpr, vpu, tat1, and rev1 genes show inactivating mutations in 64% of the clones. The data suggest that 3799 was initially infected with virulent HIV-1 but presently harbors more-attenuated viral quasispecies. Sequence set accession numbers U24443–U24487. Presumably subtype B.

HIVTH475A IIIB-TH L31963 9795 comp. gen. Neumann,M. JVI 69: 2159 (1995)
Comment: The persistently infected, low-producer human astrocytoma cell line TH4-7-5 was established by multiple rounds of cell cloning following cocultivation of parental 85HG-66 astrocytoma cells with KE37/1-IIIB cells (infected with the IIIB lab strain of HIV-1) as described in AIDS 6: 273 (1992). In this study the entire proviral genome was sequenced from TH4-7-5 cells, and the Rev and Rev responsive element (RRE) were sequenced from progeny virus rescued from TH4-7-5 glial cells into RC-2A monocyte-macrophage leukemia cells. The study indicates that the low-producer status of the TH4-7-5 glial cells is not due to a defect in Rev or the RRE, but due to cellular block of Rev-RRE-dependent regulation. Subtype B sequence.

HIV1U26942 pNL4-3 U26942 9000 comp. gen. Salminen,M.O. Virology 213, 80 (1995)
Comment: Resequencing of the complete genome of a subtype B virus, clone pNL4-3, using PCR techniques. The original sequence (M19921) was published by Akio et al. in JVI 59, 284-291 (1986). pNL4-3 is a lab-constructed hybrid of NY5 (5' half) and LAI (3' half); it is an infectious clone.

HIV1U42282 IDCON U42282 579 vif Sova,P. JVI 69: 2557 (1995)
Comment: This study sequenced vif genes from 25 individuals with varied rates of disease progression in order to determine whether intact vif is positively selected during natural HIV-1 infection and to determine vif sequence variability. A total of 46 cloned vif PCR products derived from short-term cultured virus were sequenced from five asymptomatic individuals and from five persons with AIDS. Recombinant proviruses were constructed from selected vif clones from one patient and found to be fully infectious. 38 of the 46 clones sequenced carried open vif reading frames. The cysteines previously found to be essential for vif protein function were conserved in all clones. Direct sequencing of vif PCR products from uncultured lymphocytes from another 15 individuals at various stages of progression toward AIDS, demonstrated intact vif ORFs in 13 of 15 samples tested. There was no obvious correlation between disease status and the presence of an intact vif within this sample group at the time of sample procurement. GenBank accession numbers for the complete set are: U41055-U41056, U41179-U41182, U42229-U42282. Envelope V3 regions from 3 of the first 10 individuals were also sequenced, but no GenBank entries are available.

SIU42720 Cpzant U42720 8182 comp. gen. Vanden,M. Virology (in press, 1996)
Comment: The second full sequence of a chimp immunodeficiency virus. Significantly divergent from Cpzgab, however the V3 amino acid sequences are remarkably similar. Approximately equidistant from HIV-1 group M and group O clades. Kindly provided prior to publication by Vanden Haesevelde and Saman, Innogenetics, Belgium.

HIV1U23487 MANC U23487 9655 comp. gen. Zhu,T. Nature 374, 503 (1995)
Comment: This sequence ostensibly represents HIV-1 captured by PCR from a 1959 patient known as the 'Manchester Sailor' (Corbitt,G., Bailey,A.S., and Williams,G., Lancet 336:51,(1990)). DNA provided to the Aaron Diamond AIDS Research Center for sequencing yielded this product, which is unexplainedly indistinguishable from contemporary HIV-1 sequences: all of its coding sequences cluster with subtype B sequences (for example, closely to HIVD31, GenBank Accession Number X16109) and do not reveal conspicuous synonymous substitution differences from contemporary samples. Subtype B, from U.K. Serological analysis of the HLA DQalpha marker is in disagreement with similar analysis of the 1959 patient's sample.

S74214 pNL43R(-) S74214 296 rev (RRE) Zolotukhin,A.S. JVI 68: 7944 (1994)
Comment: A mutant construct of pNL43 that is Rev(-) RRE(-). Subtype B.

| LOCUS | COMMON | ACCESSION | LENGTH | REGION | FIRST AUTHOR | REFERENCE |
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HIV1U13209 G9 U13209 543 env Abimiku,A.G. ARHR 10, 1581 (1994)
Comment: Subtype G env sequence from Nigeria that clusters with previously decribed sequences from Gabon and Zaire. Samples JV83 (U13213), JP88 (U13211), and G3 (U13208) are additional Nigerian G subtype sequences for env. For related gag sequences, see U13209 and U13212. G3 and G9 samples were from healthy prostitutes, whereas JP88 and JV83 were from AIDS patients.

HIVM01A MO1A U16390 285 env (V3) Ahmad,N. JVI 69, 1001 (1995)
Comment: Part of a set of seven mother-infant pairs from Ohio (presumably subtype B). Other M01 sequences have accession numbers U16391–U16402. The infant born to this mother is I01, represented by accession numbers U16403–U16422. Numbers for sequences belonging to the six other pairs are U16423–U16652. Most of the mothers and infants were asymptomatic. The authors argue that minor variants tend to be transmitted to the infants. PBMC samples were studied without culturing.

HIV1U10957 K11 U10957 233 env (V3) Antonioli,I.M. AIDS 9, 11 (1995)
Comment: Viral sequences from twenty-four Swiss patients were studied: sequences from individuals with primary HIV infection were compared to sequences from advanced AIDS patients. PBMC DNA and serum RNA sources were analyzed. No characteristic V3 loop sequence was found for early infections; three of the twenty-four samples possessed QRGPGR crest motifs. Presumably all subtype B sequences. Accession numbers U10957–U10980.

HIV1U23112 93–08020 U23112–U23116 1461–1497 env (partial gp120) Arnold,C. Virology 211, 198 (1995)
Comment: Sequences from three individuals in the U.K., a health-worker, a patient, and a possible sex partner of the patient. Evidence presented against the hypothesis that the health-worker infected the patient. Accession numbers U23112–U23138.

HIV1U26301 94–47621 U26301–U26303 1323 env Arnold,C. ARHR 11, 999 (1995)
Comment: G subtype sequences from a mother-infant transmission study which failed to amplify in the Roche Amplicor test. Maternal samples, 94–47621, have accession numbers U26301–U26303. Infant samples, 94–47622, have numbers U26304–U26307.

HIV1U21109 94–11643 U21109 1062 env Arnold,C. ARHR 11, 427 (1995)
Comment: At least five sequence subtypes found in the U.K.—A, B, C, D and A/E. The subtype A – A/E samples were taken from immigrants, however the subtype C and D cases may represent second-generation transmissions in the U.K. This PBL sequence and gag (U21096) and gag-pol (U21124) sequences establish the A/E subtype for sample 94–11643. Other samples in the study are: 93–08020, a subtype B (U21095, U21122, U21100); 93–43424, a subtype D (U21106, 21136, U21098); 93–00333 and 93–00513, a subtype C (Z33479, U21099); 94–31296, a subtype A (U21097). Editor's note: no pure A sequence was reported for env.

HIV1U21472 1018.2 U21472 644 env (C2–V5) Artenstein,A.W. J.I.D. 171,805 (1995)
Comment: A study of two HIV-positive individuals in Thailand, both dually infected with (harboring) B and E subtype viral forms. Other sequences from the study are U21473 (clone 1116P194.8), U21474 (1116P194.13), U21476 (1110.12), and U21471 (1018.1).

HIVU46210 BHGM19 U46210 238 env Barbosa,E.F. Unpublished
Comment: No information; possibly a Brazilian sample.

HIVHYDA HYDA L29091 267 env Baskar,P.V. ARHR 10, 1039 (1994)
Comment: Four HIV samples (amplified PBLs) from Hyderabad, India, all B subtype sequences. Accession numbers L29091–L29094. Most sera of six Hyderabad patients had cross-neutralizing activity with HIV1MN.

HIVDLU DLU U06717 1397 env (partial) Becker,M.L. ARHR 11,1265 (1995)
Comment: Fourteen samples from southern Africa (Mozambique, South Africa, Zambia and Malawi) were studied over portions of env and gag coding sequences. DLU is a 1990 isolate from South Africa, a subtype C viral sequence. Subtype B and D sequences were also uncovered, though the majority were subtype C. Related sequence accession numbers are U07011–U07018, U06716–U06719, and U07237–U07238.

HIV1U32396 QZ4589 U32396 2663 env Blattner,W. Unpublished (1995)
Comment: Single sequence, complete env cds. From Trinidad.

HIV1U08357 RU103C U08357 672 env (gp120, V3–V5) Bobkov,A. AIDS 8, 1649 (1994)
Comment: Env sequences derived from eight individuals infected in Russia and Belarus, of which one is A subtype (BL10), four are B subtype (RU109, BL3, BL5, BL6), two are C subtype (BL2, BL4), one is D subtype (BL7) as assessed mostly by HMA. Several other epidemiologically-related sequences are shown to be G subtype (RU131, RU103C, RU570, RU511 in particular). Accession numbers over the set are U08355–U08368 and U10701–U10859. See also Bobkov et al., ARHR 12:251–253,1996 for further discussion of the epidemiologically linked sequences.

HIV1U43105 GM4 U43105 1100 env(V1-V5) Bobkov,A.F. ARHR 12:169(1996)
Comment: Set of 5 envelope V3 region sequences from Gambia, GenBank accession numbers U33098-U33102, was studied. GM4, GM5 and GM7 could not be unambiguously classified. GM4, sequenced over 1.1 kB (U43105), appears to be a G/C mosaic.

HIV1U24717 Mbu1.1 U24717 319 env (V3) Briant,L. JVI 69, 3778 (1995)
Comment: Four mother-child transmission pairs from Toulouse, France were studied by analyzing 309 sequences over the V3 region. Acession numbers U24717- U25025. The data set appears to be seriously muddled, as discussed by Korber et al., Nature 378:242,1995 and by Learn et al., JVI (in press, 1996).

HIV1U12071 EP11 U12071 193 env (V4) Bryson,Y.J. NEJM 332, 833 (1995)
Comment: Sequences from an HIV-positive child at birth who subsequently appears to have cleared the virus (now seronegative and virus-negative out to five years). Accession numbers U12071–U12100, L33045–L33069.

HIVU44887 94UG019 U44887 275 env Buonaguro,L. JVI 69: 7971 (1995)
Comment: These ten envelope V3 region sequences are from PBMCs from 19 asymptomatic seropositive pregnant women from the district of Gulu in northern Uganda. A 700-bp fragment of the human immunodeficiency virus type 1 (HIV-1) env gene, including the V3-V5 region, was successfully amplified by PCR from 10 samples (52.6%) and was subsequently subjected to both a heteroduplex mobility assay for genetic screening and subtyping and DNA sequence analysis (approximately 300 bp) for nucleotide comparison and phylogenetic studies. The results show the presence of HIV-1 A and D subtypes (or clades) in this rural area, with the prevalence of the A subtype (8 of 10) being greater than that of the D (2 of 10) subtype, which is unlike what has been previously reported for Uganda. By pairwise comparison analysis, the percentage of sequence divergence among samples within each subtype is low (the average intrasubtype divergence is 15.8%); it is significantly higher between the two subtypes (the average intersubtype divergence is 23%). The 10 sequences have GenBank accession numbers U44878-U44887.

HIV1U28949 U28949 225 env (V3) Cabello,A. ARHR 11,1135 (1995)
Comment: Viral env V3 sequences from ten HIV-infected patients from Paraguay are reported; all are B subtype. Some unusual V3 crown motifs are encountered. Accession numbers U28949–U28959).

HIV1U09252 THYPD U09252 255–432 env (gp41) Calabro,M.L. ARHR 11, 11 (1995)
Comment: Thymic and PBL samples were studied from an HIV-positive Italian male. Greater V3 loop heterogeneity was observed in the thymus than in PBLs. Accession numbers U09252–U09255. B subtype V3 sequences from gp41 and V3 regions of env.

HIV1U37030 AR06 U37030 331 env (V3) Campodonico,M. ARHR 12: 79 (1996)
Comment: Sequences from fourteen residents of Rosario, Argentina having a variety of risk activities. Names between AR01 and AR56 but not all-inclusive, accession numbers U37030–U37043. Most sequences are between 260 b.p. and 340 b.p., but three are nearly 900 b.p. long: AR15 (U37043), AR16 (U37032), and AR18 (U37033). Ten of the fourteen sequences group with subtype B, three group with subtype F, and one, AR15, appears to be a B-F mosaic. Some additional samples were subtyped by HMA but were not sequenced. The authors note that although subtype B is seen among members of all risk groups, subtype F in Rosario seems to be confined to the heterosexual and IVDU populations.

HIVF12CG F12CG Z11530 9781 comp. gen. Carlini,F. J. Viral Diseases 1, 40 (1992)
Comment: HUT-78 cells infected with blood from an AIDS patient were cloned by a group in Rome, Italy. This sequence describes clone F12, which in spite of being taken from an integrated HIV-1 provirus apparently lacking any major deletions, does not release virus particles into the medium. The sequence does appear to have minor deletions, which the authors postulate could affect the correct production of viral proteins at a posttranscriptional level (see ARHR 5, 385 (1989)). Sequence F12CG clusters with subtype B and is closely related to the IIIB strain (97.4% identical to HXB2 overall, 97.6% over gag, 96.4% over pol, and 99.0% identical to HXB2 over env).

HIV1V3LOO V3LOO X84327 525 env (V3) Cohen,J.H.M. Unpublished
Comment: Two partial env sequences, accession numbers X84327 and X84328, no publication referenced in GenBank entry, not much information available. The first, X84327, is labeled "V3" by GenBank but the second, X84328, is not. Most likely subtype O—the unpublished paper cited in the GenBank entry is entitled "A novel HIV1-O strain illustrates the diversity of the O group"—and likely from France, as the first author is based there. On the other hand, there is a 1995 article in Lancet that appears to be related (Lancet 345, 856 (1995)) and which suggests that this is not an O subtype. See gag sequence HDV1GAG (X84329).

HIV1U13440 92RW008 U13440 258 env (V1–V2) Cornelissen,M. Unpublished
Comment: Sequences generated through the WHO Global Program on AIDS. Isolates were collected in Brazil, Thailand, Uganda, and Rwanda from both symptomatic and asymptomatic patients having various routes of infection. Subtypes A, B, C, D, E are represented. Sequences are commonly referred to using the short-form WHO style, XXYYZZZ, where XX is the year the isolate was collected, YY is the two-letter country code representing the nationality of the patient, and ZZZ is an isolate ID number. The majority of these isolates were collected in 1992. Most sequences are between 250 and 300 b.p. long and describe the V1–V2 region. Exceptions are 92UG037 (U15119), 92TH022 (U15120), and 92BR025 (U15121) which are complete GP160's. Sequence set accession numbers are U13440–U15121.

HIVO1V101 O1 Z47411 288 env (V1–V2) Cornelissen,M. JVI 69, 1810 (1995)
Comment: Sequences from two donor-recipient pairs The first donor and recipient are called "H" (Z47419–Z47427) and "O" (Z47411–Z47418) respectively, and the second are called "Y" (Z47448–Z47455, Z47525–Z47540) and "X" (Z47428–Z47447, Z47505–Z47524). The issue of intrapatient selection of syncytium- and non-syncytium-inducing virus phenotypes following transmission was addressed by studying two cases of accidental transmission. The authors conclude that suppression of SI viruses can be accomplished following the development of HIV-specific immunity and that the ability to suppress SI viruses does not prevent the development of immunodeficiency. All sequences presumably subtype B, all patients presumably residents of the Netherlands. The authors claim to have sequenced gag p17 and env V3 as well as env V1–V2, but all sequences in GenBank are labeled V1–V2.;

HIV1U29433 D85-40 U29433 234 env (V3) Diaz,R. ARHR (in press, 1996)
Comment: Set of 104 sequences of the V3 region. Accession numbers U29433-U29437 and U29956-U30054. According to the clone names listed in the GenBank entries, there appear to be eleven isolates representing two patients (patient "D" and patient "RA") over several years. The GenBank entries refer to a paper in press entitled "Evolution of HIV-1 in Patients Infected from the Same Source". Probably B subtype.

HIV1U11124 H1D119V4 U11124 238 env Diaz,R.S. JVI 69, 3273 (1995)
Comment: Set of 86 sequences of tat and env from a study involving three infants that received contaminated blood. Recipient 1 (R1) and recipient 2 (R2) each received blood from different donors; a third recipient (DR) received blood from both donors and became dually infected. Sequence DR106, from recipient DR, is an apparent recombinant of sequences from the separate donors. The env set includes both V3 sequences and V4/V5 sequences. GenBank accession numbers U11124-U11209. Donors and recipients all presumably American, sequences all subtype B. More details are available on 1995 compendium page III-119, entry number 82.

HIV1U17478 ASC-1 U17478 105 env (V3) Distler, O. ARHR 11, 423 (1995)
Comment: Sequences of eighteen isolates from seven males and two females, all from the general area of Sydney, Australia. Only the V3-loop cds was sequenced (105 b.p.). GenBank accession numbers U17478-U17495. All sequences subtype B and highly similar to U.S. isolates, which the authors conclude should be the basis for vaccines tested in the Sydney area,

HIV1U36859 U36859 2577 env Douglas,N.W. AIDS 10,39 (1996)
Comment: Subtype B viral sequence from U.K. (London) patient AC, clone 3. Part of a study of twelve U.K. and Ugandan isolates involving functional env gene clones. Other patient AC sample sequences have accession numbers U36860-U36864. Other B subtype sequences in this study have accession numbers U36869-U36870, U36872-U36880 and U36882. Some samples were directly sequenced, others were sequenced after co-culture. Non-B subtype sequences from this study involve A, D and A/D samples from Uganda, accession numbers U36865-U36868, U36871, U36881-U36887.

HIV1U36865 C6080-24 U36865 2577 env Douglas,N.W. AIDS 10,39 (1996)
Comment: Subtype A sequence from Uganda. Part of a study of twelve U.K. and Ugandan isolates involving functional env gene clones. Another isolate C6080 clonal sequence is U36866. Other A and D subtype sequences in this study have accession numbers U36867-U36868, U36871, U36881-U36887. Isolate UG/92/035 is reported to be an A/D mosaic (accession numbers U36881,U36883) with evidence for recombination in the vicinity of the tat/rev splice site. All isolates in this collection were cultured on PBMCs. Accession numbers for B subtype sequences in the study are U36859-U36864, U36869-U36870, U36872-U36880, and U36882.

HIVGP160EN GP160EN L42371 2565 env (gp160) Duensing,T.D. JVI 69, 7122 (1995)
Comment: Sequence from a variant cell line derived from parental cells infected with recombinant clone NL4–3 (M19921). The article includes analysis of a panel of six immunotoxin-resistant variant cell lines, four of which are derived from parental cells infected with NL4–3 and two of which are derived from cells infected with HTLV-IIIB. All six of these cell lines produce normal levels of HIV proteins and viral particles which are structurally indistinguishable from particles produced by the parent cell lines, and all produce normal levels of gp160, but in four of the six there is a a significant downregulation of cell surface gp120/gp41 and the viral particles are noninfectious. Two variant cell lines contain a single base deletion and truncation in gp41 which demonstrates the importance of gp41 for the correct processing of gp160. It is not clear from either the article or the GenBank entry exactly which cell line sequence GP160EN represents, but the GenBank entry does make a reference to overlap with NL4–3 (M19921). Both the NL4–3 and the IIIB strains are subtype B.

HIVENVFRA 89ZA500 L47608 1350 env Engelbrecht,S. ARHR 11, 1269 (1995)
Comment: Large HIV-1 env data set from South Africa, including sequences of fourteen viral strains isolated between 1984 and 1992. Sequences 87ZA509 (L48063), 87ZA510 (L48064), 87ZA524 (L48065), 88ZA512 (L48066), 88ZA513 (L48069), 85ZA504 (L48071), and 87ZA508 (L48073) are members of subtype B, sequences 92ZA517 (L48067) and 90ZA514 (L48068) are subtype C, and sequences 89ZA500 (L47608), 85ZA506 (L48061), 86ZA507 (L48062), 84ZA501 (L48070), and 85ZA505 (L48072), are subtype D. The authors postulate that HIV-1 was introduced to South Africa in parallel from North America/Europe and Africa.

HIV1U10929 SER1 U10929 210 env (V3) Furuta,Y. ARHR 10, 1187 (1994)
Comment: Sequences of the V3 region from five Swedish couples with known index cases and defined time of sexual contact, as identified by contact tracing. Transmitters indicated by the names SET1–SET5 (U10934–U10950), or simply T1–T5, and corresponding recipients by SER1–SER5 (U10929–U10933) or R1–R5. From the degree of sequence diversity observed within donor-recipient pairs, the authors conclude that either minor variants of the donor quasispecies were selected during sexual transmission, or the major variant of the donor readily mutated during initial replication in the recipient. Patients were all residents of the low-incidence city of Goteborg. All sequences presumably subtype B, because of geography and the uniform presence of the GPGR motif at the crest of the V3 loop.

HIV1U08441 91HT651.11 U08441 2821 env Gao,F. JVI In Press (1996)
Comment: The complete gp160 goding region from HIV-1 isolates collected at major epicenters of the AIDS epidemic were sequenced during a study by Gao et al., University of Alabama, Birmingham, as part of an NIH/NIAID/DAIDS study. The 38 clones from 35 individuals of this representative panel include members of all major sequence subtypes of HIV-1 group M (clades A-G) as well as an inter-subtype recombinant (F/B) from an infected individual in Brazil. In this panel, all subtype E and three subtype G viruses initially classified on the basis of partial env sequences were found to cluster in subtype A in the 3' half of their gp41 coding region, suggesting that they are also recombinant. The biological activity of of PCR derived full-length envelope genes was examined in a single round virus infectivity assay. This analysis identified 20 clones, including at least one from each subtype (or recombinant), that express fully functional envelope glycoproteins. The 20 shown to express functional env are: 92RW020.5 (U08794) subtype A from Rwanda; 92UG037.8 (U09127) subtype A from Uganda; 92BR020.4 (U08797), subtype B from Brazil; 92TH014.12 (U08801) subtype B from Thailand; 92HT593.1 (U08444) subtype B from Haiti; 92HT594.10 (U08445) subtype B from Haiti; 91HT651.11 (U08441) subtype B from Haiti; 91US712.4 (U08449) subtype B from U.S.; 92US715.6 (U08451) subtype B from U.S.; 91US006.10 (U27443) subtype B from U.S.; 91US005.11 (U27434) subtype B from U.S.; 92BR025.9 (U09126) subtype C from Brazil; 93MW965.26 (U08455) subtype C from Malawi; 92UG021.16 (U27399) subtype D from Uganda; 92UG024.2 (U43386) subtype D from Uganda; 93TH966.8 (U08456) subtype "E" from Thailand; 93TH967.17 (U08458) subtype "E" from Thailand; 93BR029.2 (U27413) subtype F from Brazil; 92UG975.10 (U27426) subtype "G" from Uganda; 93BR019.4 (U27404) subtype F/B recombinant from Brazil. Infectivity was borderline positive for 8 clones: 92HT596.4 (U08446) subtype B from Haiti; 92HT599.24 (U08447) subtype B from Haiti; 91HT652.11 (U08443) subtype B from Haiti; 92US714.1 (U08450) subtype B from U.S. (subcloning for the infectivity assay reversed a stop codon in the signal peptide of this clone); 93MW959.18 (U08453) subtype C from Malawi; 93MW960.3 (U08454) subtype C from Malawi; 93TH975.15 (U08457) subtype "E" from Thailand; 93BR020.17 (U27401) subtype F from Brazil. Infectivity was not determined for 10 clones: 92UG031.7 (L34667) subtype A from Uganda; 91HT651.1a (U08442) subtype B from Haiti; 92US657.1 (U04908) subtype B from U.S.; 92US711.14 (U08448) subtype B from U.S.; 92US716.6 (U08452) subtype B from U.S.; 93ZR001.3 (U27419) subtype D from Zaire; 92TH022.4 (U09131) subtype "E" from Thailand; 92RU131.16 and 92RU131.9 (U27445 and U30312) subtype "G" from Russia; 93BR019.10 (U27408) subtype F/B recombinant from Brazil. Thirty-seven of the clones were shown to produce envelope protein in an in vitro translation assay; 92US714.1 (U08450) contained an in-frame stop codon in the signal peptide. Many of these samples are available in the DAIDS repository. See also ARHR 10, 1359 (1994).

HIV1U14537 CJ48 U14537 241 env Gorny,M.K. JVI 68, 8312–8320 (1994)
Comment: A monoclonal antibody was developed that recognizes the V2 region of HIV-1 env. Substitutions at amino acid positions 176/177, 179/180, 183/184, and 192 to 194 in the V2 loop of env each completely abolished the binding capacity in an enzyme-linked immunosorbent assay format. The epitope was primarily conformation dependent. Oxidation of carbohydrates abolished the binding, showing the dependence of the epitope on intact carbohydrates. The V2 region of env, like the V3 region and the CD4-binding domain, can induce potent neutralizing antibodies against HIV-1 in humans. Sequence set accession numbers are U14537–U14547. Presumably subtype B.

HIV3202A12 3202A21 U34603 9636 comp. gen. Guillon,C. ARHR 11, 1537 (1995)
Comment: Two complete genomes derived from two clones from the same patient, p320, during a study of SI and NSI varients isolated from a single patient. One clone (U34603) is Syncytium Inducing while the other (U34604) is Non Syncytium Inducing. Patient p320 was from Amsterdam and probably harbors subtype B virus.

HIV1RM2 RM2 X77964 213 env (V3) Holm,C. ARHR 11, 597 (1995)
Comment: Subtype F sequences from 34 Romanian children, accession numbers X77964–X77987. Five isolates presented a syncytium-inducing phenotype in MT-2 cells and established continuous viral replication in various CD4+ cell lines. These five did not show positively charged AAs at positions 306 and 320 as has previously been shown to be correlated with an SI phenotype, but they did show a slightly more positively charged V3 loop overall.

HIVIBNG IbNg L39106 9201 comp. gen. Howard,T.M. ARHR, in press 1996
Comment: This HIV-1 subtype A strain is from a 23 year old asymptomatic male from Ibadan, Nigeria. The isolate was co-cultured in donor PBMCs for two passages before cytoplasmic RNA was harvested and RT-PCR performed to generate 5 overlapping fragments for sequencing. At least 3 separate cloned PCR products were used as sequencing templates for each of the 5 regions. The sequence presented in L39106 is a consensus of all sequencing reactions. The consensus sequence of 6–8 PCR-derived clones from the env gene was discussed in ARHR 10 (12): 1755–1757 (1994). This sequence is one of the few non-subtype B complete genomes. Some unique features were found, including a 16 bp insertion within the Lys-tRNA primer binding site (between the 5' LTR and gag) and a frameshift in the first coding exon of Tat.

HIV1U30730 50824–02 U30730 276 rev, env (gp41) Iversen,A.K.N. JVI 69, 5743 (1995)
Comment: This study substituted four complete env genes isolated from the PBMC of an asymptomatic patient 4.5 years after infection into the replication-competent NL4–3 provirus. Despite encoding full-length open reading frames for gp120 and gp41 and the second coding exon of tat and rev, each chimera was replication defective. Site-directed mutagenesis of codon 78 in the Rev activation domain (from a hitherto unique Ile, to the subtype B consensus Leu) partially restored infectivity for two of three chimeras tested. Similarly, mutagenesis of rev codon 78 of NL4–3 from Leu to Ile partially attenuated this virus. The authors also examined conservation of the Rev activation domain within and among long-term survivors (LTS) and patients with AIDS, as well as T-cell-line-adapted strains of HIV-1. Putative attenuating mutations were found in a minority of sequences from all five LTS and two of four patients with AIDS. Of the 11 T-cell-line-adapted viruses examined, none had these changes. Sequence set accession numbers U30730–U30786.

HIV1U09664 LBV21–7 U09664 2595 env Janssens,W. ARHR 10, 877 (1994)
Comment: Subtype G env sequence from Gabon. Part of a study of some of the first env genes of subtypes G and H. VI525 is another env G sequence from Gabon (U09665). CA13 and VI557 are env H subtypes from Cameroon and Zaire (U09667 and U09666 respectively). See also L22953, L11792 (VI525 Gag), L11793 (VI557 Gag), L11778 (LBV21–7 Gag). VI557 appears to be G in gag and H in env.

HIV1U12985 K971 U12985 252 env (v3) Janssens,W. ARHR 10: 1577 (1994)
Comment: Subtype A sequence from Kenya. Twenty-three isolates from 22 pregnant women and one infant (K88) from the Pumwani maternity hospital in Nairobi, Kenya are studied over the env V3 region. Accession numbers U12984–U13006. Nineteen sequences were subtype A, the other 3 were subtype D. One of the subtype A isolates (K31) was previously characterized as subtype D in gag. U12984 is K986 env subtype D, U12985 is K971 env subtype D, U12986 is K966 env subtype D, U12987 is K965 env subtype A, U12988 is K967 env subtype A, U12989 is K968 env subtype A, U12990 is K970 env subtype A, U12991 is K973 env subtype A, U12992 is K976 env subtype A, U12993 is K977 env subtype A, U12994 is K978 env subtype A, U12995 is K980 env subtype A, U12996 is K981 env subtype A, U12997 is K982 env subtype A, U12998 is K984 env subtype A, U12999 is K985 env subtype A, U13000 and L11768 are K112 env and gag subtype A, U13001 and L11771 are K31 env subtype A gag subtype D, U13002 and L11773 are K88 env and gag subtype A, U13003 and L11770 are K29 env and gag subtype A, U13004 and L11775 are K98 env and gag subtype A, U13005 is K983 env subtype A, and U13006 is K979 env subtype A.

HIVV3RE15 6–A–2 D78628 105 env (V3) Kakizawa,J. ARHR 12:561 (1996)
Comment: Subtype B sequences from the saliva of Japanese patients. Accession numbers D78614–D78637.

HIV1U22010 JWF U22010 639 env (C2-V5) Kaleebu,P. ARHR 11: 657 (1995)
Comment: This sequence is from a female who had recently immigrated from Uganda to the United Kingdom. The patient was classified as CDC stage IV and had a CD4 count of 20/mm$^3$. Subtype G.

HIV1U22543 94TH101 U22543 345 env (v3) Kalish,M.L. AIDS 9: 851 (1995)
Comment: This study characterized the env V3 region of HIV-1 from injecting drug users in Bangkok, Thailand in 1994, compared with strains found earlier. Proviral DNA from PBMCs from 84 patients in Bangkok was analyzed. Direct sequencing of PCR products was used. Only one strain was a typical subtype B virus, 69 were Thai B, and 14 were subtype E strains. Accession numbers U22542-U22626.

HIV1U15576 THP01 U15576 342 env (C2-V3) Kalish,M.L. ARHR 10: 1573 (1994)
Comment: In this study, samples were collected from thirteen consenting Thai inmates, each classified as an IDU. Of these, ten were diagnosed with infectious HIV in 1986 or 1987. The ten viral sequences were found to be similar to B subtype viruses found in Europe and the Americas. These samples were also found to be phylogenetically similar to the variants collected from IDUs infected in 1988 and 1989, however, they are distinguishable from the 1989 forms, which the authors designate B'. THP11 and THP12, from patients who were diagnosed with HIV in 1988 and 1992, were found to be subtype B' viruses, not subtype B. The remaining patient, THP13, was infected in 1989 with an E subtype virus. This subtype is predominantly found in Thai cases of sexual transmission. Kalish et al. suggest that the recent prevalence of subtypes B' and E over subtype B in Thailand may be explained by B' and E subtype infections of dynamic high-risk populations. Hence, phylogenetic comparison of Thai HIV-1 strains isolated in the mid-1980s and Thai HIV-1 strains isolated in the late 1980s indicates that the earlier virus was not responsible for the Thai epidemic beginning in 1988. U15576-U15587, THP01-THP12, are subtype B and B'; U15588, THP13, is subtype E.

HIVAV3AAG BL1033.4 Z23177 233 env (V3) Keys,B. Virology 196: 475 (1993)
Comment: In this study envelope V3 region sequences taken from the blood of 7 patients were compared to sequences from the CSF of the same patients. No correlation was found between tissue type and V3 sequences. Z23177, Z23182-Z23184 subtype A from Uganda; Z23178-Z23181, Z23185-Z23187, Z23192-Z23195, Z23200-Z23203, Z23204-Z23215 subtype B from Sweden; Z23192-Z23199 subtype C from Zimbabwe.

HIV1ENVKR KR-121 X93469 220 env Kim,Y.B. Unpublished
Comment: X93469; no information available yet.

HIVU45960 JR-CSF 17.11 U45960 3211 vpu, env, nef Klasse,P.J. ARHR 12: 347 (1996)
Comment: Syncytium-inducing mutant clone of isolate JR-CSF. Subtype B.

HIV1U05360 1BL287 U05360 163 env Korber,B.T.M. JVI 68: 7467 (1994)
Comment: This study looked at differences in the envelope C2-V5 region in HIV-1 isolates derived from blood vs. isolates derived from brain tissue in HIV-1 infected individuals. Sequences from blood and brain samples of six patients with acute, rather than chronic, HIV-related neurological disease were analyzed. Patients 1-4 were sampled in 1990 and 5-6 were sampled in 1992. Eight to 36 clones from each sample were sequenced. Brain-derived V3-loop sequences showed lower intrapatient diversity than blood-derived V3-loop sequences. The limitation in brain-derived sequences may be related to macrophage-monocyte tropism of the brain-derived sequences. U05360-U05568, subtype B from U.S..

HIV1U28661 CYHO024 U28661 384 env (C2-C4) Kostrikis,L.G. JVI 69: 6122 (1995)
Comment: This study looked at envelope C2-V3 region sequences from 24 HIV-1-seropositive patients from Cyprus. Heteroduplex mobility assays showed that HIV-1 gp120 sequences from 15 patients were of subtype B, one was of subtype C and eight patients had no obvious similarities to the known subtypes as defined by HMA. DNA sequenes placed the eight undefined HIV-1 isolates into three distinct genetic clusters. One group consisting of three clones from two patients was provisionally designated subtype I. The remaining two were distally related to subtypes A and F. U28661-U28685, U28719 and U28321, subtypes A, B, C, F and I.

HIVSER149 SER149 Z37937 276 env (V3) Kuiken,C.L. J. Gen. Virol. 76: 175 (1995)
Comment: In this study, envelope V3-region sequences from blood and CSF samples from 4 AIDS patients with and 8 without AIDS dementia complex (ADC) were studied. A significant ADC-associated difference occurring at several amino acid positions was noted. Results from serum and CSF sequences were comparable. Accession numbers Z37531-Z37963, Z37970-Z37971, subtype B from the Netherlands.

HIVL466 L466 Z29256 276 env (V3) Kuiken,C.L. PNAS 90: 9061 (1993)
Comment: Sequence variations in the envelope V3-loop region were studied in 74 newly infected individuals from three Dutch cohorts: 30 homosexual men, 32 drug users, and 12 hemophiliacs. Samples were collected between 1980 and 1991. The V3-loop variability increased over time in both the homosexual and the drug-user risk groups. Accession numbers Z29220-Z29225, Z29256-Z29325, subtype B from the Netherlands.

HIVH0001L H0001L Z67875 270 env (V3) Kuiken,L. AIDS In Press (1996)
Comment: No information available yet. Z67875-Z67876, Z67885-Z67960, Z68015-Z68089, Z68109-Z68110 subtype B from the Netherlands.

HIVJGV10 P4664 Z68508 276 env Kuiken,L. J. Gen. Virol. In press (1996)
Comment: Title = "Consistent risk group-associated differences in HIV-1 vpr, vpu and V3 sequences despite independent evolution". This is a set of 117 vpu and envelope V3 region sequences from Dutch, Scottish and German patients belonging to different risk groups. GenBank accession numbers for the complete set are Z68505, Z68508-Z68616, and Z68687-Z68693.

HIV17887E SE7887E L41176 255 env (V3) Leitner,T.K. ARHR 11: 995 (1995)
Comment: Two unrelated individuals who immigrated to Sweden from Zaire had concordant env and gag sequences, which provisionally define a new subtype J. L41176-L41177 are env sequences, L41178-L41179 are gag. Subtype J, Zaire (Sweden).

HIV16165E SE6165E L40743 264 env (V3) Leitner,T.K. Virology 209: 136 (1995)
Comment: In this study three Swedish HIV-1 transmission chains of subtypes other than subtype B were characterized. The three index cases were African men. Gag and env V3 regions were directly sequenced from uncultured lymphocytes. One group harbored subtype D, another subtype G and the third a recombinant gag-D/env-A subtype. The culture phenotype of virus (SI or NSI) correlated with the clinical stage of the infected individual suggesting that the correlation between biological phenotype and V3 genotype that has been established for subtype B variants may also be valid for other subtypes. L40743-L40751 env; L40752-L40760 gag; L40761-L40763 pol. Subtypes G, D and gag-D/env-A (recombinant) from Sweden.

HIV1U24562 BCF02 U24562 261 env Loussert,I. JVI 69: 5640 (1995)
Comment: Sequences encoding Gag p24 and the Env C2-V3 region were obtained from seven patients who were seronegative with ELISA detection kits and had atypical Western blot reactivity. Sequence analyses showed that all of these strains were group O. All seven patients had Cameroonian origins but were living in France at the time the blood samples were taken. Genetic distances between sequences from available group O isolates were generally comparable to those observed in M intersubtype sequence comparisons. U24562-U24568 env; U24706-U24712 gag. Group O, from France.

HIV1BZ126A BZ126 L22082 3312 tat, rev, vpu, env, nef Louwagie,J. ARHR 10, 561 (1994)
Comment: Env subtype F sequence from Brazil. Part of a study of twenty-one seropositive Brazilians sampled for virus in 1989–1990. B and F subtype sequences were recovered. BZ200 (L22088) and BZ167 (L22087) are B subtype sequences, BZ163 (L22085) and BZ162 (L22084) are other F subtype sequences. The subtype B V3-loop crown sequences were unusual, as has been found for other Brazilian sequences. The BZ126 gag sequence presented in L22083, does not group with subtype F as it did in the publication. Instead it appears to be an A/C recombinant, suggesting a data entry mixup. Accession numbers L11751–L11754 are related.

HIV1SE364A SN364 L22944 3110 tat, rev, vpu, env, nef Louwagie,J.J. JVI 69, 263 (1995)
Comment: Subtype C sequence from Senegal. Full-length env gp160 sequences were obtained from isolates from 8 African countries. Subtype A, C, D, and G sequences are reported. Samples were collected between 1989 and 1991. ZM184 was most closely related to subtype A sequences, but distant enough to warrant an “unclassified” designation. Accession numbers L22939–L22957, L23064, L23065.

HIV1RUS2A RUS2 L38404 270 env Lukashov,V.V. AIDS 9, 435 (1995)
Comment: Sequences from Russia, Byelorussia and Lithuania. Subtype B (homosexually–infected men) and C (heterosexually–infected men) sequences are reported. Accession numbers L38404–L38420.

HIV1U40285 RU190 U40285 450 env Malykh,A.G. Unpublished (1996)
Comment: This set of 17 envelope V3 region sequences from St. Petersburg, Russia has not yet been published. No information is available. GenBank accession numbers for the entire set are U40283-U40285, U40319-U40330 and X56086-X56087.

HIV1U09992 353 U09992 105 env (V3) Mammano,F. JVI 69, 82 (1995)
Comment: U09992–U10015. Sequences of the env V3 loop from 24 infants from Padua, Italy, who were perinatally infected with HIV-1, were correlated with patient health and viral culture characteristics. The consensus or direct sequence of PCR products is presented in GenBank, but numerous individual clones were also sequenced. All isolates were similar to subtype B, but the sequences are too short to make a definitive identification of subtype.

HIV1BWB BWB-1 L17088 1002 env Monken,C.E. AIDS 9, 345 (1995)
Comment: Subtype B sequences from the U.S. Fifty clones, PCR amplified from the brain tissue of a single patient. Thirty-nine unique nucleotide sequences producing 35 protein variants were found. Sequences varied from the consensus by 0.1–2.1% at the nucleotide level. The number of N-linked glycosylation sites varied. No inactivating mutations were found. Accession numbers L17088–L17126.

HIVMA MA-114 L21028 276 env (V3) Mulder,G.A. J. Gen. Virol. 74: 1747 (1993)
Comment: Three mother-child pairs were studied. For pair 114 the infant was HIV positive at birth, for pair 127 the infant became positive 6 weeks after birth and the infant of pair 564 became positive 30 months after birth. Mothers 127 and 114 were seropositive before giving birth. Mother 564 seroconverted after delivery and the infant was infected via breast-feeding. For V3 and p17gag sequences, maternal intrasample variability, including the first seropositive sample of the seroconverted mother, was much higher than infant intrasample variability. In each case the infant was infected by a minor variant present in the maternal sequences. The sequences of the env and gag genes did not identify a particular time of mother-to-child transmission. L21111-L21153 are infant 114 env subtype B from the Netherlands; L21028-L21110 are mother 114 env subtype B from the Netherlands; Z47817-Z47832 are infant 127 env subtype G from the Netherlands; Z47833-Z47880 are mother 127 env subtype G from the Netherlands; Z47881 is child 564 env subtype A from Rwanda; Z47882-Z47902are mother 564 env subtype A from Rwanda; Gag gene sequences from mother/child pairs are also available in Genbank accession numbers Z47903-Z47911; Z47912-Z47928; Z47929-Z47935; Z47936-Z47950. See also Mulder-Kampinga,G.A. et al. JVI 69, 2285 (1995)

HIVTH475A IIIB-TH L31963 9795 comp. gen. Neumann,M. JVI 69: 2159 (1995)
Comment: The persistently infected, low-producer human astrocytoma cell line TH4-7-5 was established by multiple rounds of cell cloning following cocultivation of parental 85HG-66 astrocytoma cells with KE37/1-IIIB cells (infected with the IIIB lab strain of HIV-1) as described in AIDS 6: 273 (1992). In this study the entire proviral genome was sequenced from TH4-7-5 cells, and the Rev and Rev responsive element (RRE) were sequenced from progeny virus rescued from TH4-7-5 glial cells into RC-2A monocyte-macrophage leukemia cells. The study indicates that the low-producer status of the TH4-7-5 glial cells is not due to a defect in Rev or the RRE, but due to cellular block of Rev-RRE-dependent regulation. Subtype B sequence.

HIV1U39233 BU/91/01 U39233 2547 env Penny,M.A. ARHR (in press, 1996)
Comment: Subtype C viral sequence from Burundi; from isolate BU/91/01 selected from the WHO-NHIC repository at NIBSC, Potters Bar, U.K. Part of a study of full-length expression-competent env gene clones (see Douglas et al., AIDS 10:39,1996). U39252 is another clonal sequence from isolate BU/91/01. BU/91/02–BU/91/08 are other isolates producing functional C subtype sequences in this study (accession numbers U39237, U39239–U39251, U39257).

HIV1U39253 BU/91/09 U39253 2547 env Penny,M.A. ARHR (in press, 1996)
Comment: Unidentified subtype sequence from Burundi; from isolate BU/91/09 selected from the WHO-NHIC repository at NIBSC, Potters Bar, U.K. Part of a study of full-length expression-competent env gene clones (see Douglas et al., AIDS 10:39, 1996). U39254 is another clonal sequence from isolate BU/91/09.

HIV1U39234 BR/91/15 U39234 2580 env Penny,M.A. ARHR (in press, 1996)
Comment: Subtype C viral sequence from Brazil; from isolate BR/91/15 selected from the WHO-NHIC repository at NIBSC, Potters Bar, U.K. Part of a study of full-length expression-competent env gene clones (see Douglas et al., AIDS 10:39,1996). U39238 is another clonal sequence from isolate BR/91/15.

HIV1U39235 BR/93/29 U39235 2547 env Penny,M.A. ARHR (in press, 1996)
Comment: Subtype F viral sequence from Brazil; from isolate BR/93/29 selected from the WHO-NHIC repository at NIBSC, Potters Bar, U.K. Part of a study of full-length expression-competent env gene clones (see Douglas et al., AIDS 10:39,1996). U39236 is another clonal sequence from isolate BR/93/29.

HIV1U39258 TH/93/67 U39258 2520 env Penny,M.A. ARHR (in press, 1996)
Comment: Subtype B (B') viral sequence from Thailand; from isolate TH/93/67 selected from the WHO-NHIC repository at NIBSC, Potters Bar, U.K. Part of a study of full-length expression-competent env gene clones (see Douglas et al., AIDS 10:39, 1996). U39259 is another clonal sequence from isolate TH/93/67.

HIV1U39260 TH/92/01 U39260 2556 env Penny,M.A. ARHR (in press, 1996)
Comment: Subtype E viral sequence from Thailand; from isolate TH/92/01 selected from the WHO-NHIC repository at NIBSC, Potters Bar, U.K. Part of a study of full-length expression-competent env gene clones (see Douglas et al., AIDS 10:39, 1996). U39256 is another clonal sequence from isolate TH/92/01. U39255 and U39261 are other subtype E sequences, from isolate TH/92/11, generated in this study.

HIV1U11586 ARTC1 U11586 635 env (V3, C2-V5) Pestano,G.A. ARHR 11, 589 (1995
Comment: Two U.S. subtype B sequences used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. Both patients were intravenous drug users from New York. ARTC1 (U11586-U11589) was asymptomatic and ARTC3 (U11590-U1194) had AIDS. For related sequences see U11595-U11599.

HIV1U11595 UG042p U11595 655 env (V3, C2-V5 Pestano,G.A. ARHR 11, 589 (1995)
Comment: Five Ugandan subtype D sequences (U11595-U11599) used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. All five patients were asymptomatic blood donors. For related sequences see U11586-U11594.

HIV1U16764 VE1 U16764 1425 env (V3) Quinones,M.E. ARHR 11, 605 (1995)
Comment: Eight Venezuelan subtype B sequences (U16764-U16779) derived from PCR amplified PBMCs taken from eight different patients (VE1-VE8). Despite the close geographical proximity of the patients, this study reports significant heterogeneity.

HIV1U12030 LW851 U12030 2691 env Reitz,M. ARHR 10: 1143 (1994)
Comment: Sequences from a U.S. labworker accidentally infected with IIIB virus. Accession numbers U12030–U12055. Subtype B.

HIV1ENVB ENVB L23090 369 env (V3) Reitz,M. ARHR 10: 621 (1994)
Comment: Subtype B sequences from some of the earliest isolates in the U.S. For other sequences, see accession numbers L23091–L23103. Subtype B.

HIVU43099 P104 U43099 886 env Reitz,M. Unpublished (1990)
Comment: A set of Zairean sequences from blood samples collected in 1983-1985 from AIDS patients in Kinshasa, and from healthy seropositive paratroopers outside of Kinshasa, Zaire. U43097-U340100 are subtype A. U43101-U43102 are subtype C.

HIV1U28283 DRAB U28283 180 env Rencher,S.D. ARHR 11, 1131 (1995)
Comment: Thirty-eight sequences of the envelope V1-V2 region and V3 loop, were obtained from two individuals, A and B. Patient A had tested HIV negative 2 months prior to sampling, and was asymptomatic. Patient B was also asymptomatic, and the seroconversion date is unknown. Serum from patient A neutralized a IIIB lab strain of HIV, but failed to neutralize a primary isolate. Serum from patient B neutralized IIIB and two different primary isolates. The greater sequence diversity and the greater neutralizing capacity seen in patient B were consistent a with longer period of HIV infection than patient A. Accession numbers U28313-U28320 and U28283-U28293. Subtype B samples from the U.S.

HIV1EN1 EN1 Z29681 204 env Rojas,J.M. Virus Res. 31, 331 (1994)
Comment: Thirteen Spanish subtype B sequences (Z29681-Z29692 Z29919) from different patients. Rojas et al. identify two distint lineages within the cohort. One lineage is related to SF-2/RF and is epidemiologically linked to male homosexuals, while the second, related to III-B, is linked to intravenous drug users. For related gag sequences see Z29693-Z29701.

HIVU47806 U47806 663 env (C2–V5) Roth,W.W. ARHR (in press, 1996)
Comment: Eleven HIV-infected mothers from the U.S. and their babies were studied. Three of the babies are shown to be HIV-positive at 27 months, 5 months, and 21 months. Subtype B sequences, accession numbers U47783–U47807.

HIV1U23216 R2235 U23216 304 env (v3) Saah, A. Unpublished
Comment: Seventy-one subtype A sequences from Rwanda including isolates R2235 (U23216-U23234, U23255-U23263), R1831 (U23235, U23236, U23238, U23283-U23294, U23353-U23372), R1613 (U23237, U23239-U23254, U23295, U23296, U23304-U23308, U23313-U23319, U23323-U23325, U23332-U23333), R561 (U23264-U23282, U23334-U23352, U23373), R1701 (U23297-U23303, U23309-U23312, U23320-U23322, U23326-U23331).

HIV1U08953 U08953 282 env (V3) Sabino,E.C. JVI 68, 6340 (1994)
Comment: Thirty-two Brazilian sequences from a study documenting B-F recombinants. Sample RJ548 (U08955-U08964) was obtained from a Brazilian man and samples RJ549 (U08965-U08971) and RJIO1 (U08972, U08973) were taken from his female sexual partner. Sabino et al. maintain that these two patients harbor B-F recombinant HIV-1. Sample RJIO3 (U08974) was taken from a Brazilian woman with subtype F HIV-1.

HIV1U20670 U20670 1601 env (gp120) Sala,M. ARHR 11, 653 (1995)
Comment: Subtype B sequences obtained from Langerhans cells from skin patches of a deceased Italian AIDS victim who was a doubly infected intravenous drug user. For related sequences see Z34304-Z34515.

HIVENV RI Z34304 280 env (V3) Sala,M. JVI 68, 5280 (1994)
Comment: Subtype B sequences (Z34304-Z34515) obtained from Langerhans cells from skin patches of a deceased Italian AIDS victim who was a doubly infected intravenous drug user. For related sequences see U20670-U20677.

HIV1U26942 pNL4-3 U26942 9000 comp. gen. Salminen,M.O. Virology 213, 80 (1995)
Comment: Resequencing of the complete genome of a subtype B virus, clone pNL4-3, using PCR techniques. The original sequence (M19921) was published by Akio et al. in JVI 59, 284-291 (1986). pNL4-3 is a lab-constructed hybrid of NY5 (5' half) and LAI (3' half); it is an infectious clone.

HIV1U20001 CR7 U20001 360 env (C2-V3) Shao,Y. Unpublished (1995)
Comment: Fifty-four sequences isolated from Chinese asymptomatic individuals with normal CD4 counts, Yunnan province, mostly subtype B sequences. Accession numbers U20001–U20054.

HIV1U16063 XSH144C U16063 1048 env (V1-V5) Shapshak,P. Adv. Exp. Med. Biol. 373, 225
Comment: Seventy-six subtype B sequences from the U.S. used in a study of the role of HIV-1 in the complications of AIDS. To this end Shapshak et al. examined PBMCs, brain cells, and CSF from three intravenous drug users: patients 141 (U16032-U16062), 144 (U16063-U16093), and 149 (U16094-U16117). The suffixes R, L, and C indicate Brain, PBMC, and CSF respectively. The data set appears to contain problematic sequences as discussed by Learn et al., J. Virol. (in press, 1996).

HIV1GUN GUN-1 D34590-D34600 105 env (V3) Shimizu,N.S. J. Virol. 68, 6130 (1994)
Comment: Twenty-two probable subtype B sequences from three isolates GUN-1 (D34590-D34600), GUN-4 (D34601-D34606), and GUN-7 (D34607-D34611). All three were from Japanese hemophiliacs and were used in a study of HIV-1 variants infectious to brain-derived cells. The three isolates each proved to be infectious to brain-derived cells and mutations of proline to serine, alanine, or threonine occured in each. Shimizu et al. believe that this indicates the importance of amino acid sequences at the tip of the V3 region for brain cell tropism of HIV-1.

HIV1U23651 86NE357 U23651 612 env (V3) Shpaer,E.G. ARHR 10, 1679 (1994)
Comment: Sequences of fifty-seven subtype B samples (U23651-U23708) taken from patients in the Netherlands and the U.S. close to the time of seroconversion. Part of a study of conserved V3 loop sequences and the transmission of HIV-1. Shpaer et al. found that the cysteine-bridged V3 loops of these sequences were highly conserved and that the regions surrounding it were highly divergent.

HIV1U00804 MACB91–01 U00804 618 env Shpaer,E.G. Unpublished
Comment: Accession numbers U00804–U00850. No information available.

HIV1U12406 TZ005 U12406 1372 env (V1–V3) Siwka,W. ARHR 10: 1753 (1994)
Comment: Ten samples from Tanzania, sequenced over vpU and env V1–V3. Eight samples yielded D subtype sequences, two A subtype sequences. Accession numbers U12406–U12415.

HIV1U22682 Infant A U22682 282 env (V3) Strunnikova,N. JVI 69, 7548 (1995)
Comment: One-hundred and twenty-nine U.S. subtype B sequences from six infants: Infant A (U22682-U22689 U22702-U22704), Infant B (U22690-U22701), Infant C (U22705-U22720), Infant D (U22721-U22736 U22834), Infant E (U22737-U22776), and Infant F (U22777-U22810). Part of a study of the correlation of genetic variation of the V3 region with disease progression.

HIV1U29179 IND1 U29179 1488 env (gp120) Tripathy,S.P. ARHR (in press, 1996)
Comment: Nine patient samples from India, three from New Delhi and six from Pune. Eight yield subtype C sequences (U29179, U29694-U29698, UU31362, UU31363) and one (from New Delhi) yields a subtype B sequence (U31364).

HIVGT1 GT1 D13420 204 env (V3) Tsuchie,H. Jpn. J. Med. Sci. Biol. 46, 95 (1993)
Comment: Eight Indian sequences (D13420-D13427) derived during a study of the V3 loop of HIV-1 strains in India. The V3 loops of seven of the isolates sequenced contained the apical tetrapeptide GPGQ while the remaining one contained the apical tetrapeptide GPGK. The same seven (highly similar) sequences clustered with the C subtype.

HIV1U32205 U32205 198 env (V1-V2) Vallejo,A. ARHR 11:1539 (1995)
Comment: Two sequences (U32205, U32206) from a seronegative AIDS patient, presumably subtype B.

HIV1U13264 ACH1140 U13264 105 env (V3) van 't Wout,A.B. J. Clin. Invest. 94: 2060 (1994)
Comment: A simple method for the isolation and subsequent detection of human immunodeficiency virus type 1 (HIV-1) RNA from feces is described. The method was applied on fecal specimens from 18 HIV-1-infected individuals, among which were samples that had been stored for 9 years. HIV-1 RNA was detectable in the feces of 12 persons (67%). Viral RNA was present in the feces of persons who fulfilled the criteria for CDC class II and CDC class III HIV infection as well as in patients who were diagnosed with AIDS (CDC class IV). Direct sequencing of amplimers obtained from paired fecal and serum specimens showed that differences in sequence heterogeneity existed. In one patient a remarkable difference in the HIV-1 sequences between isolates from feces and serum was observed. Presumably subtype B sequences from the Netherlands, accession numbers L38720-L38733.

SIU42720 Cpzant U42720 8182 comp. gen. Vanden,M. Virology (in press, 1996)
Comment: The second full sequence of a chimp immunodeficiency virus. Significantly divergent from Cpzgab, however the V3 amino acid sequences are remarkably similar. Approximately equidistant from HIV-1 group M and group O clades. Kindly provided prior to publication by Vanden Haesevelde and Saman, Innogenetics, Belgium.

HIV1U15005 U15005 222 env (V3) von Brunn,A. ARHR 11, 183 (1995)
Comment: Three Ugandan sequences from a set of HIV-1 viral isolates from Africa. All three individuals from which the virus was cultured had AIDS, and the year of viral isolation was 1987. Viruses were cultured with HUT-78 cells for an unspecified length of time. The V3 region of env (gp160) was amplified, cloned and sequenced. GenBank accession numbers U15005, U15006 and U15007. Subtype D, from Kampala, Uganda.

HIV1U19621 038C U19621 314 env (V1-V2) Wang,N. JVI 69, 2708 (1995)
Comment: Fifty-seven subtype B sequences (U19621-U19677) from forty-seven patients. Samples were taken from North America, Australia, and Haiti during an investigation of sequence diversity in V1 and V2 domains of gp120. Wang et al. found that there was no correlation between V1 or V2 sequences and the viral phenotype.

HIV1U16324 CB7 U16324 1005 env Wang,W.-K. ARHR 11, 185 (1995)
Comment: Twelve subtype B sequences (U16324-U16335) from a U.S. patient. Wang et al. identify two uncommon cysteine residues in the hypervariable V1 loop of gp 120. These added residues have been encountered in HIV-2 and SIV sequences.

HIV1U19694 CB1I171 U19694 924 env (gp120) Wang,W.-K. Unpublished
Comment: Eighteen sequences (U19694-U19711) from nine U.S. patients, CB1-CB9. CB7 samples appear to be from the same patient yielding sequences U16324-U16335.

HIV1U35901 P1134 U35901 659 env Wolinsky,S.M. Unpublished (1996)
Comment: This is a set of 292 envelope V2-V5 region sequences related to longitudinal study of HIV genetic variation and its relation to rate of disease progression. These patients are from the Chicago MACS cohort. In the study, P1 and P2 were rapid progressors, P3 and P4 normal progressors, and P5 and P6 non-progressors. Their estimated years of seroconversion are as follows: for P1, 1985, for P2, 1985, for P3, 1986, for P4, 1986, for P5, 1984, and for P6, 1985. In the sample number, Px.y-z, x stands for the patient number, y is the number of months after the estimated date of seroconversion, and z is the clone number.; THe complete set includes GenBank accession numbers U35894-U36185.

HIV1U15030 68A U15030 2574 env (V3) Wrin,T. JVI 69, 39 (1995)
Comment: A group of three Dutch subtype B sequences from the same patient. Wrin et al. adapted isolate ACH168.10, presumably the same as isolate 68p (U15032), to growth in the FDA/H9 cell line. 168A (U15030) is a sequence of the same virus four weeks after the beginning of the experiment and 168C cell adapted virus (U15031) is a sequence at the completion of the adaptation. The adaptation made the virus sensitive to neutralization by vaccine sera.

HIV1U10583 C-001 U10583 162 env (V3) Yamashita,A. Virology 204, 170 (1994)
Comment: Forty-six sequences from three Japanese patients: C-175 (U10583-U10595), C-148 (U10596-U10617), and C-001 (U10618-U10628). Using these sequences, Yamashita et al. found that macrophage-tropic virus is homogenous in monocytes/macrophages and has a common V3 structure in contrast to T-cell-tropic virus in vivo. Presumably subtype B.

HIV1U25550 CMU01A3 U25550 303 env Yu,X.F. JVI 69, 4649 (1995)
Comment: Seventy-seven Thai subtype E sequences (U25550-U25626) used in a study of the phenotypic and genotypic characteristics of HIV-1 from patients in northern Thailand. Of the twenty-two AIDS patients involved in the study, sixteen were found through the use of MT-2 cells to be SI phenotype. Yu et al. determined that characteristics of amino acid sequences in V3 associated with the subtype E HIV-1 SI phenotype are unique and have not been reported for subtype B SI forms.

HIV1U16372 UD1 U16372 1047 env Zhu,T. JVI 69, 1324 (1995)
Comment: Put forth as evidence that coinfection by multiple HIV-1 strains can occur in vivo, these subtype B sequences come from an Australian homosexual male harboring three distinguishable populations as well as mosaics of the three sequence variants. Sequence set accession numbers U16372–U16388.

HIV1U16373 UD2 U16373 1041 env Zhu,T. JVI 69, 1324 (1995)
Comment: Envelope sequences from plasma and PBMCs collected over four time points from an acute seroconvertor showed that the patient harbored three distinct populations of HIV-1 clade B envelope sequences, with nucleotide distances ranging from 9.2 to 17.2%. One population of sequences was clearly distinguishable from the others on the basis of phylogenetic analysis. In addition, sequences suggesting recombination between two of the three distinct viral populations were also found. This case of acute seroconversion provides clear and conclusive evidence that coinfection by multiple HIV-1 strains can indeed occur in vivo. Sequence set accession numbers U16372-U16388.

HIV1U23487 MANC U23487 9655 comp. gen. Zhu,T. Nature 374, 503 (1995)
Comment: This sequence ostensibly represents HIV-1 captured by PCR from a 1959 patient known as the 'Manchester Sailor' (Corbitt,G., Bailey,A.S., and Williams,G., Lancet 336:51,(1990)). DNA provided to the Aaron Diamond AIDS Research Center for sequencing yielded this product, which is unexplainedly indistinguishable from contemporary HIV-1 sequences: all of its coding sequences cluster with subtype B sequences (for example, closely to HIVD31, GenBank Accession Number X16109) and do not reveal conspicuous synonymous substitution differences from contemporary samples. Subtype B, from U.K. Serological analysis of the HLA DQalpha marker is in disagreement with similar analysis of the 1959 patient's sample.

**HIV-1 NEF Sequence Summaries**

| LOCUS | COMMON | ACCESSION | LENGTH | REGION | FIRST AUTHOR | REFERENCE |
|---|---|---|---|---|---|---|

HIVF12CG F12CG Z11530 9781 comp. gen. Carlini,F. J. Viral Diseases 1, 40 (1992)
Comment: HUT-78 cells infected with blood from an AIDS patient were cloned by a group in Rome, Italy. This sequence describes clone F12, which in spite of being taken from an integrated HIV-1 provirus apparently lacking any major deletions, does not release virus particles into the medium. The sequence does appear to have minor deletions, which the authors postulate could affect the correct production of viral proteins at a posttranscriptional level (see ARHR 5, 385 (1989)). Sequence F12CG clusters with subtype B and is closely related to the IIIB strain (97.4% identical to HXB2 overall, 97.6% over gag, 96.4% over pol, and 99.0% identical to HXB2 over env).

HIV1U37267 C18 U37267 493 ltr, nef Deacon,N.J. Science 270, 988 (1995)
Comment: Sequences relating to an Australian blood donor infected with HIV-1 and six Australian recipients, all of whom remain symptom free with normal CD4 counts 10 to 14 years after infection. Samples from only the donor, D36 (U37271), and two patients, C18 (U37267, U37270) and C98 (U37268, U37269), appear to have been sequenced. These sequences have similar deletions in the nef gene and in the region of overlap of nef and the U3 region of LTR. The authors point to the importance of NEF or the U3 region of LTR in determining the pathogenicity of HIV-1 and suggest this strain of HIV-1 as a possible basis for a live attenuated vaccine. Presumably subtype B.

HIV3202A12 3202A21 U34603 9636 comp. gen. Guillon,C. ARHR 11, 1537 (1995)
Comment: Two complete genomes derived from two clones from the same patient, p320, during a study of SI and NSI varients isolated from a single patient. One clone (U34603) is Syncytium Inducing while the other (U34604) is Non Syncytium Inducing. Patient p320 was from Amsterdam and probably harbors subtype B virus.

HIVNEF1 NEF1 X63040 628 nef Harris,M. ARHR 8, 537 (1992)
Comment: Subtype B. Six HIV-1 nef genes from PBMC DNA of asymptomatic seropositive individuals were analyzed. Nef1 and Nef6 had premature terminations, Nef2 and Nef3 had mutations at sites of potential posttranslational modification. Other accession numbers are X63041–X63045.;

HIVIBNG IbNg L39106 9201 comp. gen. Howard,T.M. ARHR, in press 1996
Comment: This HIV-1 subtype A strain is from a 23 year old asymptomatic male from Ibadan, Nigeria. The isolate was co-cultured in donor PBMCs for two passages before cytoplasmic RNA was harvested and RT-PCR performed to generate 5 overlapping fragments for sequencing. At least 3 separate cloned PCR products were used as sequencing templates for each of the 5 regions. The sequence presented in L39106 is a consensus of all sequencing reactions. The consensus sequence of 6–8 PCR-derived clones from the env gene was discussed in ARHR 10 (12): 1755–1757 (1994). This sequence is one of the few non-subtype B complete genomes. Some unique features were found, including a 16 bp insertion within the Lys-tRNA primer binding site (between the 5' LTR and gag) and a frameshift in the first coding exon of Tat.

HIV1U16863 BO1 U16863 621 nef Huang,Y. JVI 69, 93 (1995)
Comment: The HIV-1 nef gene was sequenced from 10 patients who were clinically healthy and immunologically normal despite 12 to 15 years of infection. There was no gross deletion within nef in the cases studied; most nef sequences (91.1%) obtained from the 10 subjects contained a full-length and intact open reading frame. In addition, at the protein level, there were no discernible differences between the Nef consensus sequences derived from long-term survivors and those from patients with AIDS. Presumably subtype B sequences. Accession numbers U16863–U16952.

HIV1U17438 COLDO U17438 176 nef Kirchhoff,F. N. Engl. J. Med. 332: 228 (1995)
Comment: This study found defective nef open reading frames in a long-term non-progressor. U17438-U17472, subtype B viral sequence from the U.S.

HIVU45960 JR-CSF 17.11 U45960 3211 vpu, env, nef Klasse,P.J. ARHR 12: 347 (1996)
Comment: Syncytium-inducing mutant clone of isolate JR-CSF. Subtype B.

HIV1BZ126A BZ126 L22082 3312 tat, rev, vpu, env, nef Louwagie,J. ARHR 10, 561 (1994)
Comment: Env subtype F sequence from Brazil. Part of a study of twenty-one seropositive Brazilians sampled for virus in 1989–1990. B and F subtype sequences were recovered. BZ200 (L22088) and BZ167 (L22087) are B subtype sequences, BZ163 (L22085) and BZ162 (L22084) are other F subtype sequences. The subtype B V3-loop crown sequences were unusual, as has been found for other Brazilian sequences. The BZ126 gag sequence presented in L22083, does not group with subtype F as it did in the publication. Instead it appears to be an A/C recombinant, suggesting a data entry mixup. Accession numbers L11751–L11754 are related.

HIV1SE364A SN364 L22944 3110 tat, rev, vpu, env, nef Louwagie,J.J. JVI 69, 263 (1995)
Comment: Subtype C sequence from Senegal. Full-length env gp160 sequences were obtained from isolates from 8 African countries. Subtype A, C, D, and G sequences are reported. Samples were collected between 1989 and 1991. ZM184 was most closely related to subtype A sequences, but distant enough to warrant an "unclassified" designation. Accession numbers L22939–L22957, L23064, L23065.

HIV1U26060 50069 U26060 618 nef Michael,N.L. JVI 69, 6758 (1995)
Comment: HIV-1 nef genes from nine patients with highly divergent rates of disease progression were sequenced. During the study period (7.8 years avg per patient), three patients had net positive changes in CD4+ T-cell counts, three patients had net negative changes in CD4+ T cells but did not develop AIDS, and three patients progressed to AIDS. Only 2.3% of the nef genes recovered from these nine patients were grossly defective. There was no correlation between nef sequences and rate of disease progression. Sequence set accession numbers U26060–U26147. Presumably subtype B.

HIVTH475A IIIB-TH L31963 9795 comp. gen. Neumann,M. JVI 69: 2159 (1995)
Comment: The persistently infected, low-producer human astrocytoma cell line TH4-7-5 was established by multiple rounds of cell cloning following cocultivation of parental 85HG-66 astrocytoma cells with KE37/1-IIIB cells (infected with the IIIB lab strain of HIV-1) as described in AIDS 6: 273 (1992). In this study the entire proviral genome was sequenced from TH4-7-5 cells, and the Rev and Rev responsive element (RRE) were sequenced from progeny virus rescued from TH4-7-5 glial cells into RC-2A monocyte-macrophage leukemia cells. The study indicates that the low-producer status of the TH4-7-5 glial cells is not due to a defect in Rev or the RRE, but due to cellular block of Rev-RRE-dependent regulation. Subtype B sequence.

HIV1U26942 pNL4-3 U26942 9000 comp. gen. Salminen,M.O. Virology 213, 80 (1995)
Comment: Resequencing of the complete genome of a subtype B virus, clone pNL4-3, using PCR techniques. The original sequence (M19921) was published by Akio et al. in JVI 59, 284-291 (1986). pNL4-3 is a lab-constructed hybrid of NY5 (5' half) and LAI (3' half); it is an infectious clone.

SIU42720 Cpzant U42720 8182 comp. gen. Vanden,M. Virology (in press, 1996)
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Comment: This sequence ostensibly represents HIV-1 captured by PCR from a 1959 patient known as the 'Manchester Sailor' (Corbitt,G., Bailey,A.S., and Williams,G., Lancet 336:51,(1990)). DNA provided to the Aaron Diamond AIDS Research Center for sequencing yielded this product, which is unexplainedly indistinguishable from contemporary HIV-1 sequences: all of its coding sequences cluster with subtype B sequences (for example, closely to HIVD31, GenBank Accession Number X16109) and do not reveal conspicuous synonymous substitution differences from contemporary samples. Subtype B, from U.K. Serological analysis of the HLA DQalpha marker is in disagreement with similar analysis of the 1959 patient's sample.